

DASZAK: MALTHUSIAN CRYPTO-ECO-FASCIST WHO INTENTIONALLY ORCHESTRATED SARS-2 PANDEMIC

[This former Congressional Researcher contracted Covid-19 in March 2000.](#) The medics had to beat on my chest to bring me back to life. I was in Lenox-Hill Hospital for a month with a lung tube. The disease left one of my fingers paralyzed making it hard to type correctly. I did research which boils down to this: Peter Cottonton Daszak *deliberately and intentionally* caused a pandemic by finacing all the players, convincing them they work working on a vaccine for the next SARS outbreak then ignoring warning signs of a leak that would be apparent to anyone with his credentials; such as ignoring the fact the experiments and bat virus storage were in a BSL-2 lab with as much safety as a dentists office. It's all here, all referenced with live links to sources, but thanks to the Democratic Party, and the corporate media that keeps them in power, it will be ignored. Even if you believe there was no hidden agenda and if it was just a case gross negligence Daszak still should be tried. [This is a draft of a bi-partisan committee to investigate the cause of the pandemic.](#)

OR WORLD CLASS CONMAN?

DASZAK JUNE 2020: "I gave a talk at a government meeting, and the OSTP, the Office of Science and Technology Policy, Director was there from the White House, Franca Jones," Daszak begins while outlining his efforts to identify and sequence all viruses with pandemic potential. "I kind of faked it a little bit. I said, look, I've got a piece of paper here with a number," he continues before appearing to backtrack: "I did actually... we just calculated the day before." So I had this piece of paper, and I kind of pulled it out and it says 'it will only cost 7 billion dollars,' and I saw her write down the number. I thought wow, this isn't so crazy," he added. Commander Franca Jones – who is listed on the White House visitor logs reviewed by The National Pulse – was the director of medical programs for the Department of Defense's chemical and biological defense program. Under Jones's tenure, the Defense Department shipped live anthrax spores to labs in several U.S. states and military bases.

69945	DAstorg	Gwenola	2/26/2013 10:25	2/26/2013 23:59	OFFICE	VISITORS	WH	RESIDENCE
69946	Dasu	Sridhara	3/15/2013 13:00	3/15/2013 23:59	Rubin	Philip	OEOB	442
69947	Daszak	Peter	2/21/2013 9:00	2/21/2013 23:59	Jones	Franca	OEOB	472
69948	Datcher	Linda	11/5/2013 11:30	11/5/2013 23:59	OFFICE	VISITORS	WH	RESIDENCE
69949	Date	Rajeev	1/24/2013 14:00	1/24/2013 23:59	Hogan	Nancy	WH	WW 1st Flo

CHAPTER 1**EVIDENCE DASZAK ORCHESTRATED THE PANDEMIC****FAMILY TREE**

Peter Cottonton Daszak (pronounced "Daysh-ak,") is a war criminal like his Nazi father, Bohdan, who was a member of the Youth Section of the Ukrainian Nazi party. As one would expect Bohdan volunteered to be an executioner at the Janowska German Nazi death camp combining elements of labor, transit, and extermination camps. It was established in September 1941 on the outskirts of Lwów in Eastern Poland / Western Ukraine. Inmates: Jews Liberated by: The Red Army Operated by: SS. Bohdan was captured by the British and sent to the UK where he was released into the UK population because if was deported to the Ukraine he would be hung, as well he should have been. Bohdan married Ruth Alice Mary Walton. Ian Walton and David Walton of Dukinfield Sons of Ian Walton, also of Dukinfield. AF Police for one, if not both - I think Ian was a dog handler. Grandfather was John Walton. Grandmother **Ruth Alice Mary Walton** (both of of Dewsnap lane) Aunt was Ruth Daszak [Wikitree](#) Bohdan died on February 1996 in

Tameside, Greater Manchester, England, where he had worked in Hill's Biscuit Factory. Ruth, a Brit, gave birth to Peter in 1969. There is a DOB listed in his Wiki profile. England & Wales, Civil Registration Marriage Index, 1916-2005 Peter Daszak Spouse [Janet D.C.](#) [Go to Table of Contents](#) [7] Daszak is a Ukrainian Brit expat with a Phd in Zoology specializing in parasites that attack reptiles. Daszak is not a microbiologist and he was he doing financing and personally conducting of experiments with bat viruses at the Wuhan Institute of Virology with Fauci's funding? Daszak is slick con man and wormed his way in to Fauci and USG A.I.D. circles despite lack of real credentials. He is Malthusian Eco-Fascist spook determined decrease human population in favor of Flora and Fauna.

- Daszak hides his past: His brother John, told a biographer that his father, Bohdan was a Nazi death camp guard in the Ukraine however Daszak claims Bohdan was inscripted into the Nazi Army. Daszak was raised by a mass murderer, a hardcore Nazi and was indoctrinated by Bohdan in Nazi ideology. This gave him a basis to justify mass murder. Daszak is a crypto-Nazi. [MORE ON BOHDAN](#)
- Daszak is an agent-of-influence for the Nazi-like Chinese Communist Party, that rounds-up Muslims and puts them in concentration camps and forced work camps and re-education camps. Note: Although aligned with the Democratic party, and pretending to be a liberal Democrat, he never mentions CCP human rights abuses.
- Daszak visited and worked at the scene of the crime before Covid was first reported. Wuhan China was where the pandemic first started, only CCP stooges deny it.
- Daszak financed the collection of viruses found in bat blood, feces and urine, some of which might be deadly to humans, if they "spilled-over" from nature directly to humans or through an intermediate species. He stored them in BSL-2 lab at the Wuhan Institute of Virology (WIV) that has the same bio-security as a dentist's office. Daszak and Shi Zeng-Li's collection numbers more than 20,000 batsamples. But Shi explained that on average only 10% contain coronaviruses, and only 10% of those are closely related to SARS-CoV-1: in all its years, the team has identified approximately 220 suchviruses.
- The process of culturing viruses involves providing them with cells they can infect. Several labs around the world have tried to get live bat coronaviruses and failed. Until <https://www.nature.com/articles/s41467-020-20458-9> target="_blank"> [January 2021](#), the Wuhan lab was the only one that had managed the feat, according to Stephen Goldstein, a coronavirus expert at the University of Utah in Salt Lake City. Yang Xinglou, a senior research scientist on Shi's team worked on this.
- Daszak intentionally orchestrated the pandemic by financing and initiating dangerous gain-of-function, gain-of-threat experiments with corona bat viruses at the WIV by repurposing NIH grants to WIV. [See for yourself where you taxpayer money went](#) Obama banned these procedures in the USA. Daszak outsourced NIH grants from Fauci and his Deputy, Erik Stemmy to Shi Zeng Li, his anally fixated micro-biologist asset, who believes "The pandemic is nature's punishment for an *unsanitary lifestyle*." This faceless, mentally ill, robot was Head of Security at the WIV. Why was Daszak so determined to continue these Gain-of Threat experiment? Because he knew they would leak and cause a pandemic.
- The experiments he financed were aimed at enhancing Corona virus spike proteins, some found in horseshoe bats that caused the first SARS mini-pandemic, to more easily invade the ACE2 cells in the human lung. "We sequenced the spine protein, the protein that attaches to cells, and then you create pseudo particles, insert proteins from the viruses that combined to human cells. Each step of this you move closer and closer to could the virus becomes pathogenic in people! You narrow down the field. You end up with a small number of viruses that really do look like killers."
- Daszak knew a virus would having a good chance of leaking from the BSL-2 WIV lab built in 1956 and never reported it. How did he know other than his conducting experiments there himself? The US State Department had visited the BSL-4 lab built by the French (for experiments with viruses that had no vaccine or cure) and reported major defects in security - so you can imagine what the BSL-2 lab was like.
- He introduced Shi Zeng Li to Ralph Baric, a cowboy microbiologist known as "Mr. Gain-of-Function," who developed a method to disguise the fact a virus had been genetically altered, among other things. Baric also developed a method to bring viruses of the past, such as polio, back, through reverse genetic engineering. So a virus could never be wiped off the planet as long as its nucleic code existed. Baric once gave a lecture on how to profit from a pandemic. [Baric screwed-up](#) and caused a minor pandemic in the area of the University of North Carolina.
- On New Years Day 2019 Daszak was one of the first people in the USA to know of the existence of COVID-19 from his asset at the WIV, Shi Zeng Li. He was first on the scene of the crime.
- DASZAK covered-up his own crime when Daszak led the WHO investigation and cover-up in China that suggested the virus came from Barcelona via frozen meat. Daszak was not allowed on the second WHO panel because of a "conflict-of-interest" due to his WIV connection. "It can take years or even decades to find the cause of a new infectious disease. Sometimes we just never know."
- Daszak tried to cover up the lab leak theory by orchestrating a letter from various micro-biologists, many of whom were on Fauci's grant pad, that did not contain his name. The claimed the virus spilled over from nature. Daszak also became a fact-checker at Facebook, which permanently banned this researcher from advertising.
- Daszak had a good cover story to disguise his hidden agenda. Dr. Daszak ran the semi-governmental PREDICT program which was supposed to *predict pandemics* and got millions of dollars from numerous USG agencies, even from the Department of Fish and Wildlife. He convinced Baric and Li that they were conducting gain-of-threat experiments to see which bat virus was next to spillover from nature so they could develop a vaccine for it before it became a pandemic. In the venacular, he "chumped them off."
- Daszak planned to genetically enhance airborne coronaviruses and release aerosols containing nano particles with "novel chimeric spike proteins" among cave bats in Yunnan, China. He was going to do the same with MERS viruses which are 30% more deadly than SARS-19. DARPA refused to fund these experiments because of the danger of creating a pandemic.
- [DASZAK co-authored an Eco-Fascist Manifesto that depicted animals destroying humans.](#)
- Daszak co-authored a paper with [A. J. Wakefield](#), an anti-vaxxer whose medical license was revoked. Convincing people not to get vaccinated is a Malthusian work-around to cut down human population by exposing them to disease. See [A. J. Wakefield](#) for more.
- [Daszak still insists there was no lab leak despite the FBI's finding to the contrary.](#)
- [Fauci lied under oath and covered up for Daszak when he denied NIH never funded Gain-of-Threat research: Daszak authored a paper](#) stating "This summary contains the information for the 2014 and 2017 NIH and NIAID grants to the Ecohealth Alliance that funded the WIV research on bat coronaviruses. As the grant description shows, this research included gain-of-function / gain-of-threat research to make coronaviruses viruses more pathogenic using techniques including genetic engineering, cell culture, and animal experimentation."
- Daszak labeled anyone who attributed the pandemic to a lab leak as a "conspiracy theorist." There is no conspiracy here. Daszak played these microbiologists like a violin.

- Daszak violated the law regarding grant subrecipients that required him to "Monitor the activities of the subrecipient as necessary to ensure that the subaward is used for authorized purposes, in compliance with Federal statutes, regulations, and the terms and conditions of the subaward." Daszak allowed gain-of-function, gain-of-threat experiments that were illegal in the US when he repurposed his Fauci / Stemmy grants
- Daszak: June 6, 2014 "We will use Spike Protein1 sequence data, infectious clone technology,2 in vitro and in vivo3 infection experiments and analysis of receptor binding to test the hypothesis that % divergence thresholds in Spike Protein sequences predict spillover potential. We will combine these data with bat host distribution, viral diversity and phylogeny, human survey of risk behaviors and illness, and serology to identify SARS-CoV spillover risk hotspots across southern China." Do the words "spike protein" ring any bells?
- One of Daszak's papers was entitled [GIVING A SARS-LIKE VIRUS THE ABILITY TO INFECT HUMANS](#)
- The former vice-President of ECO-Health [Andrew Huff](#) is bonkers or pretending to be: "For the past 2 months I have been under constant surveillance in all forms, my house has been broken into, hard drives have been stolen, electronic eavesdropping equipment has been installed throughout my home, all my electronic devices have been hacked with drones, culminating with being attacked in my house with microwaves from an aircraft."
- The virus has genocidal characteristic: researchers have found that the coronavirus infects both fat cells and certain immune cells within body fat, prompting a damaging defensive response in the body. The United States has one of the highest rates of obesity in the world. Most American adults are overweight, and 42 percent have obesity. Black, Hispanic, Native American and Alaska Native people in the U.S. have higher obesity rates than white adults and Asian Americans; they have also been disproportionately affected by the pandemic, with death rates roughly double those of white Americans.
- Why would Daszak risk his daughter's life by doing this? Seventy-five percent of people who have died of the virus in the United States — or about 600,000 of the nearly 800,000 who have perished so far — have been 65 or older. One in 100 older Americans has died from the virus. For people younger than 65, that ratio is closer to 1 in 1,400.
- "To monitor New York City for the presence of novel variants, we deep sequence most of the receptor binding domain coding sequence of the **S protein of SARS-CoV-2** isolated from the New York City wastewater. Here we report detecting increasing frequencies of novel cryptic SARS-CoV-2 lineages. Cryptic lineages detected from wastewater are resistant to some neutralizing antibodies." [Nature](#)
- [Daszak blocked disclosure of Covid-19-relevant virus data from China as you can see from the email below.](#)

From: Peter Daszak
Sent: Tuesday, April 28, 2020 11:30 AM
To: 'Hongying Li' <li@ecohealthalliance.org>; Tammie O'Rourke <torourke@metabiota.com>
Cc: Goldstein, Tracey <tgoldstein@ucdavis.edu>; Aleksei Chmura <chmura@ecohealthalliance.org>; Christine Kreuder Johnson <ckjohnson@ucdavis.edu>
Subject: RE: China Genbank Sequences
Importance: High

All – It's extremely important that we don't have these sequences as part of our PREDICT release to Genbank at this point.

As you may have heard, these were part of a grant just terminated by NIH.

<https://www.politico.com/news/2020/04/27/trump-cuts-research-bat-human-virus-china-213076>

Having them as part of PREDICT will bring very unwelcome attention to UC Davis, PREDICT and USAID.

Cheers,

Peter

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 CC: [Goldstein, Tracy](#) [Alekseia Chmura](#) [Christine Kreuder Johnson](#)

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<https://www.politico.com/news/2020/04/27/trump-cuts-research-bat-human-virus-china-213076> Having them as part of PREDICT will bring very unwanted attention to UC Davis, PREDICT and USAID.

Cheers, Peter

PROFILES OF DASZAK'S DUPES MENTIONED IN THIS EMAIL



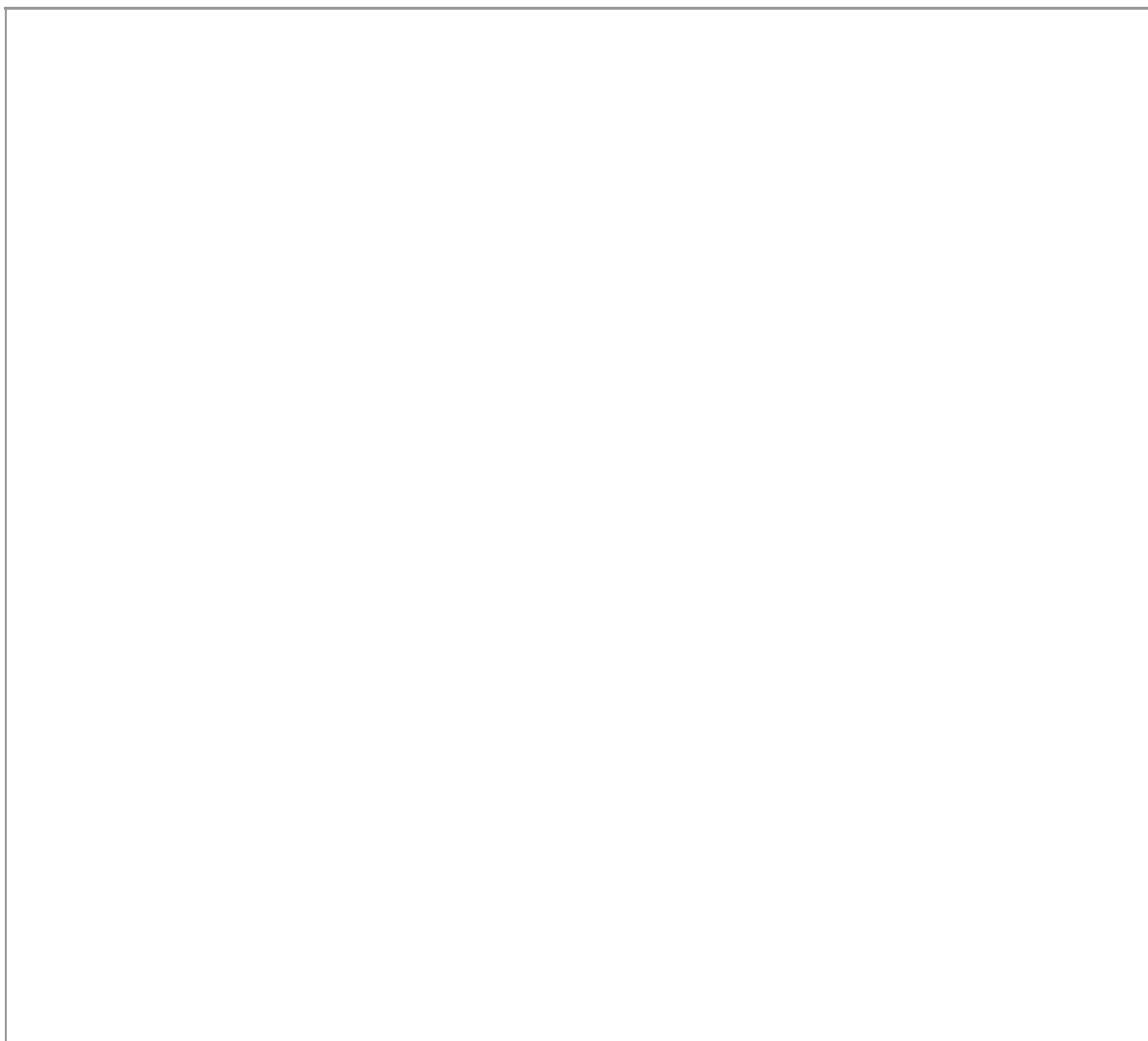
[DASZAK EXPLORES THE LAB LEAK THEORY](#)

Dr. Daszak: "This summary contains the information for the 2014 and 2017 NIH and NIAID grants to the Ecohealth Alliance that funded the WIV research on bat coronaviruses. As the grant description shows, this research included gain-of-function / gain-of-threat research to make coronaviruses viruses more pathogenic using techniques including genetic engineering, cell culture, and animal experimentation." [Source of](#)

[document: Covid-references-International Center for Technology Assessment](#)

Dr. Fauci told Rand Paul: "Senator, with all due respect, you are entirely and completely incorrect, that the N.I.H. has not ever and does not now fund gain-of-function research in the Wuhan Institute." The N.I.H. used Daszak as its surrogate to do this. To hold Daszak responsible means holding Fauci responsible which the Democrats and Corporate Media will not do.

<https://www.nytimes.com/2021/06/20/science/covid-lab-leak-wuhan.html>



file:///C:/Users/AKimbrell/AppData/Local/Microsoft/Windows/INetCache/Content.Outlook/M37O4WG
0/PLOS%202017%20China%20Bat%20SARS%20CV%20ppat.1006698%20(002).pdf

This entry (above) refers to <https://journals.plos.org/plospathogens/article?id=10.1371/journal.ppat.1006698> DATED **NOVEMBER 30, 2017**: Daszak claimed this experiment was funded by USAID, NIH etc. This is a lie. It was funded by the ChiComs. Ben Hu, Lei-Ping Zeng, Xing-Lou Yang, Xing-Yi Ge, Wei Zhang, Bei Li, Jia-Zheng Xie, Xu-Rui Shen, Yun-Zhi Zhang, Ning Wang, Dong-Sheng Luo, Xiao-Shuang Zheng, Mei-Niang Wang, Peter Daszak, Lin-Fa Wang, Jie Cui, Zheng-Li Shi.

HOW THE CIA PREDICTED THE PANDEMIC



APRIL 2016 THOUSAND PAGE CIA PROPRIETARY REPORT SUPPORTED OBAMA'S BAN ON GAIN-OF-FUNCTION / GAIN OF THREAT RESEARCH IN USA

Most estimates of the transmissibility of the coronaviruses consider these pathogens to be insufficiently transmissible and sufficiently susceptible to control measures such that a global pandemic has a very minimal chance of occurring. **For this reason, increasing the transmissibility of the coronaviruses could significantly increase the chance of a global pandemic due to a laboratory accident. Because SARS-CoV is more transmissible than MERS-CoV, a relatively modest increase in transmissibility of SARS-CoV could increase risk, whereas MERS-CoV must be made significantly more transmissible to drive risk.** That being said, even if these strains were modified to be as transmissible as pandemic influenza, the susceptibility to control measures of the outbreaks they cause would still

contain a majority of the outbreaks initiated. Some researchers have posited that the transmissibility of wild type SARS-CoV is quite high. If they are correct, then increasing the transmissibility of SARS-CoV would not influence risk significantly because the risk of a global pandemic arising from an outbreak is already significant. Increasing the pathogenicity of these strains could also increase risk somewhat through the increase in global deaths expected, especially since most deaths from wild type strains are suffered by those with significant co-morbidities. However, if a coronavirus were modified such that it caused a global pandemic, their long incubation time and disease course lead to a pandemic that unfolds over many years. The fact that the outbreak evolves slowly gives public health authorities more time to adapt and expand their efforts to further contain the outbreak than the modeling conducted in this assessment suggests. **If a strain with enhanced growth properties was developed and samples with 1E9pfu/ml or 1E10pfu/ml were routinely manipulated in a laboratory, the risk of a laboratory acquired infection in a coronavirus laboratory would increase by up to ten-fold, respectively.** However, it is uncertain if this phenotype is desirable or even achievable given that the wild type coronaviruses grow sufficiently well in culture.

Robert A. Heber Chairman at Gryphon International, Inc. YOU NEVER RETIRE FROM THE AGENCY

Mr. Heber's aviation career began in 1965 as a U.S. Army aviator and continued to serve in the Army Reserves and attained the rank of Major in the Military Intelligence Branch. In 1971, Mr. Heber continued his civilian education and earned his Bachelor of Science Degree in Aeronautical Science with a minor in Aviation Management, as well as an Associate of Arts Degree in Business Administration. His commercial aviation career began with the Cessna Aircraft Company as a Regional Marketing Manager, where he was responsible for the marketing of Cessna single and multi-engine aircraft and the development of Cessna dealerships and pilot training enters. He continued his aviation career from 1974 to 1979 with the Central Intelligence Agency where he was assigned as an Intelligence Officer within the Directorate of Operations/Special Operations Group. He has had experience in counter-terrorism, counter-narcotics, para-military operations, as well as the overt and covert collection of intelligence. His additional responsibilities included assignment as the Liaison Officer to the Federal Bureau of Investigation and the Immigration & Naturalization Service. During this period of time he developed lasting contacts, both domestically and internationally, that have been invaluable to him in his business career. Mr. Heber does have a current TOP SECRET security and is a Special Investigator retained by the United States Government Department of Homeland Security. Mr. Heber is also a licensed Private Investigator with the State of Florida.



DASZAK ROUND-UP

[WAP editorial Leftwing Annenberg Foundation and Big Pharma Johnson & Johnson attack lab leak theory China reports on Congressional investigation FOLLOW BILLY BOSTICKSON ON TWITTER. DRASTIC...Scientist who wrote anti-lab-leak-letter on Fauci's pad...Daszak and FBI Intercept Article...Smithsonian Funding Daszak?...Unredacted Email about supression of leak theory...Biden Admin still funding Daszak...EcoHealth Alliance CEO Peter Daszak just got another taxpayer-funded windfall. Instead of being deposed regarding his firm's work at the Wuhan Institute of Virology, he is receiving a new pile of cash from the United States Agency for International Development \(USAID\). The new award gives EcoHealth Alliance \\$4.675.023 for a five-year project in Liberia, on the continent of Africa....Yuri Deigin An appeal for an objective, open, and transparent scientific debate about the origin of SARS-CoV-2](#)

Rep. Yvette Herrell: Bill to Protect Tax Money From Funding Adversaries <https://t.co/4FoskuQ6Qd> via @news_ntd

— A. J. Weberman (@AJWeberman) February 13, 2022

CHAPTER 9

DISCOVERY OF A RICH GENE POOL OF BAT SARS-RELATED CORONAVIRUSES PROVIDES NEW INSIGHTS INTO THE ORIGIN OF SARS CORONAVIRUS

THIS DISCOVERY INSPIRED THE FRENCH TO BUILD THE BSL-4 LAB AT THE WIV

"Construction of recombinant viruses: **Recombinant viruses with the S gene of the novel bat SARSr-CoVs and the backbone of the infectious clone of SARSr-CoV WIV1 were constructed using the reverse genetic system described previously.** The fragments E and F were re-amplified with primer pairs...The fragment Es and Fs were both digested with BglI (NEB) and BsaI (NEB). The Rs4231 S gene was digested with BsmBI. The Rs7327 S gene was digested with BsaI. The other fragments and bacterial artificial chromosome (BAC) were prepared as described previously. Then the two prepared spike DNA fragments were separately inserted into BAC with Es, Fs and other fragments. The correct infectious BAC clones were screened. The chimeric viruses¹ were rescued as described previously." (Deborah A. Kimbrell is Associate Research Geneticist Emerita and Lecturer Unit Department of Molecular and Cellular Biology, College of Biological Sciences U of C Davis).

1. A chimeric virus is a genetic chimerism or chimera is a single organism composed of cells with more than one distinct genotype. These experiments were creating novel viruses like the SARS-CoV19N.

ECO-FASCISM - TAKING ECOLOGY ONE STEP BEYOND RATIONALITY

Doctor "Daszakstein" wanted to see a pandemic engulf humanity to [cut down human population](#) in favor of vegetation and animal life, so he convinced Fauci, USAID, Pentagon and others to fund his PREDICT PROGRAM. This is why Daszak will never embrace the lab-leak theory, because he would be incriminating himself. DASZAK: "The implications of wildlife EIDs (Emerging Infectious Diseases) are twofold: emerging *wildlife diseases cause direct and indirect loss of biodiversity and add to the threat of zoonotic disease emergence. Since human environmental changes are largely responsible for their emergence, the threats wildlife EIDs pose to biodiversity and human health represent yet another consequence of anthropogenic influence on ecosystems. More and more people are also living and working closer to wildlife. It isn't about one or two individuals putting people at risk. The risk also comes from clear-cutting rainforests, remote mining, and even widespread suburbanization.*" Anthropogenic means caused by humans. Daszak tweeted this to [IBPES](#). "Most pandemics are linked to wildlife and human-caused environmental change, such as deforestation and wildlife trade." His Zoonotic spill-over from nature cover-story, however, fell apart after "an allied power," (probably France who built the BSL-4 LAB at the WIV), determined several scientists became contaminated with an enhanced SARS virus and brought it, within their bodies, into Wuhan, during its incubation period and after the FBI determined with moderate certainty there was a lab leak.

DASZAK KILLED AND SICKENED SO MANY HUMAN BEINGS HE IS THE NEW HITLER

How could one man cause all this havoc? He is a cunning psychopathic zoologist, although he is sometimes listed as a parasitologist. The lab leak theory has been entwined with politics, rather than science, thanks to Donald Trump who promulgated the theory alongside his bleach drinking remedy, and thanks to Fauci, who has become a target of anti-vaccination types and who must resign or be fired, because he approved Daszak's experiments. Daszak could have blown the whistle on the dangerous conditions at the WIV, cut their funding, and prevented the pandemic, instead he did just the opposite. He didn't do a thing because he is an Eco-Fascist who wanted a pandemic. He must be given a fair trial in USDC/SDNY then face [the federal death penalty](#). There is precedent for charging Daszak: A Brazilian congressional panel recommend President Jair Bolsonaro be charged with "crimes against humanity," asserting that he intentionally let the coronavirus rip through the country and kill hundreds of thousands in a failed bid to achieve herd immunity and revive Latin America's largest economy. He was blamed for 300,000 deaths [NYT](#)

MINOR VIOLATIONS OF LAW

Daszak violated the law regarding grant subrecipients that required him to **"Monitor the activities of the subrecipient as necessary to ensure that the subaward is used for authorized purposes, in compliance with Federal statutes, regulations, and the terms and conditions of the subaward;** and that subaward performance goals are achieved. Pass-through entity monitoring of the subrecipient must include: (1) Providing subrecipients with training and technical assistance on program-related matters; and (2) Performing on-site reviews of the subrecipient's program operations; (3) Arranging for agreed-upon-procedures engagements as described in § 75.425.

https://www.govregs.com/regulations/title45_chapterA_part75_subpartD_subjgrp28_section75.352

In order to receive the grant Daszak had to sign-off on this declaration: "I am aware that any false, fictitious, or fraudulent information, or the omission of any material fact, may subject me to criminal, civil or administrative penalties for fraud, false statements, false claims or otherwise. (U.S. Code Title 18, Section 1001 and Title 31, Sections 3729-3730 and 3801-3812)." There is no statute of limitations for embezzlement of federal money. Fauci knew where the money was going - straight to the WIV to conduct these "maligned" experiments that Fauci thought might save mankind. Fauci let this GoF research out-sourcing go down. Program Officer Erik J Stemmy probably didn't approve Daszak's grants without showing them to his boss, Fauci. But it was Peter Daszak who caused the pandemic that setback humanity for decades.



Just as Robert Kennedy Jr., an environmental lawyer, uses anti-vaccination propaganda to increase the human death rate, Daszak uses his "small non-profit," as Dr. Fauci calls it, [the Eco-Health Alliance](#), to do the same. Also see [Also see robertkennedyjr.org](#)





ROBERT F. KENNEDY JR. TOP / PETER DASZAK BOTTOM

FOR ECO-FASCISTS LIKE RFK JR - COVID-19 IS A BLESSING

CHAPTER 2

THE EXPERIMENTS

IS THIS WHAT HAPPENED? "AN UNEXPECTED RESULT OF THE RESEARCH, AS OPPOSED TO SOMETHING THAT THE RESEARCHERS SET OUT TO DO" (LIKE CAUSE THE PANDEMIC)

The limited experiment described in the final progress report provided by EcoHealth Alliance was testing if spike proteins from naturally occurring bat coronaviruses circulating in China were capable of binding to the human ACE2 receptor in a mouse model. All other aspects of the mice, including the immune system, remained unchanged. In this limited experiment, laboratory mice infected with the SHC014 WIV1 bat coronavirus became sicker than those infected with the WIV1 bat coronavirus. As sometimes occurs in science, this was an unexpected result of the research, as opposed to something that the researchers set out to do. Regardless, the viruses being studied under this grant were genetically very distant from SARS-CoV-2. The research plan was reviewed by NIH in advance of funding, and NIH determined that it did not fit the definition of research involving enhanced pathogens of pandemic potential (ePPP) because these bat coronaviruses had not been shown to infect humans. As such, the research was not subject to departmental review under the HHS P3CO Framework. However, out of an abundance of caution and as an additional layer of oversight, language was included in the terms and conditions of the grant award to EcoHealth that outlined criteria for a secondary review, such as a requirement that the grantee report immediately a one log increase in growth. These measures would prompt a secondary review to determine whether the research aims should be re-evaluated or new biosafety measures should be enacted. EcoHealth failed to report this finding right away, as was required by the terms of the grant. EcoHealth is being notified that they have five days from today to submit to NIH any and all unpublished data from the experiments and work conducted under this award. Additional compliance efforts continue. [Lawrence A. Tabak, D.D.S., Ph.D. Principal Deputy Director](#)

Dr. Tabak is the principal deputy director of the National Institutes of Health (NIH) and the deputy ethics counselor of the Agency. He previously served as acting principal deputy director of NIH (2009), and prior to that as director of the National Institute of Dental and Craniofacial Research from 2000-2010. Prior to joining NIH, Dr. Tabak was the senior associate dean for Research and professor of [Dentistry](#) and Biochemistry & Biophysics in the School of Medicine and Dentistry at the University of Rochester in New York. A former NIH MERIT recipient, Dr. Tabak's major research focus has been on the structure, biosynthesis and function of glycoproteins. Also see [New York Times Bat Research Group Failed to Submit Virus Studies Promptly, N.I.H. Says](#)

TABAK LETTER FROM COMMITTEE ON ENERGY AND COMMERCE

We write to continue our oversight of National Institutes of Health (NIH) grant awards to EcoHealth Alliance (EcoHealth). On January 6, 2022, the NIH sent two letters to EcoHealth related to its failure to comply with terms agreed upon for its NIH grants.¹ While we appreciate the NIH's current enforcement efforts to obtain EcoHealth's compliance, new information from recently disclosed information included in the recent NIH letters raises troubling concerns about EcoHealth's conduct upon which the NIH is either overlooking or taking insufficient action. Those concerns include withheld data and possible double billing, missing laboratory notebooks and electronic files related to humanized mice research at the Wuhan lab, and EcoHealth's private donations that may not have been reported to NIH. These concerns raise the prospect of possible fraud that require the NIH's heightened attention. In June 2014 and during the gain-of-function research pause in the United States, NIH awarded grant R01AI110964 to EcoHealth for bat coronavirus research. EcoHealth then entered into a subaward agreement with scientists at the Wuhan Institute of Virology (WIV) for research assistance. During that time, EcoHealth also received awards from other U.S. agencies, including as a subgrant recipient from the U.S. Agency for International Development (USAID) to support scientific collaboration at the WIV.² Through its USAID project work, EcoHealth catalogued human and bat genomic sequence findings into a database used to create predictive maps of potential disease outbreaks and reported finding a high number of SARS-like coronaviruses in bats sampled in China.³ EcoHealth identified several novel bat coronaviruses.⁴ USAID also supported sampling by EcoHealth and its collaborative partners of more than 7,300 humans and animals in China. The human specimens were obtained from individuals with symptoms of an infectious disease meeting criteria that the most-likely cause had been ruled out through laboratory tests and supporting data was available. [READ THE REST OF THIS LETTER](#)

EARLIER EXPERIMENTS INVOLVED THE SPIKE PROTEINS WHICH ARE THE KEYS TO INVADING THE HUMAN RESPIRATORY SYSTEM

IN VITRO AND IN VIVO CHARACTERIZATION OF SARS-COV SPILLOVER RISK, COUPLED WITH SPATIAL AND PHYLOGENETIC ANALYSES TO IDENTIFY THE REGIONS AND VIRUSES OF PUBLIC HEALTH CONCERN (DASZAK)

JUNE 6, 2014 "We will use Spike Protein¹ sequence data, *infectious clone* technology,² in vitro and in vivo³ infection experiments and analysis of

receptor binding to test the hypothesis that % divergence thresholds in Spike Protein sequences predict spillover potential. We will combine these data with bat host distribution, viral diversity and phylogeny, human survey of risk behaviors and illness, and serology to identify SARSr-CoV spillover risk hotspots across **southern China**. Together these data and analyses will be critical for the future development of public health interventions and enhanced surveillance to prevent the re-emergence of SARS or the emergence of a **novel SARSr-CoV**. Project Start 2014-06-01 / Project End 2020-04-24 / Budget Start 2019-07-24 / Budget End 2020-04-24 / Support Year 6 / Fiscal Year 2019 / Total Cost / **Indirect Cost**" <https://grantome.com/grant/NIH/R01-AI110964-06>

1. The spike protein is what gives the Corona Virus its unique name. It is the part of the virus that plugs into the ACE2 receptors in human lungs and allows the nano-particle to infect the human body just like plugging a USB cord into a port on your computer.

2. Infectious clones of viral genomes were initially produced in the late 1970s and early 1980s. The first was made in 1978 by inserting a DNA copy of the RNA genome of the bacteriophage QB, made with reverse transcriptase, into a plasmid vector. Infectious virus was produced when the cloned viral DNA was inserted into *E. coli*. In 1980, infectious cloned retroviral DNA was produced by inserting the integrated viral DNA from the cellular genome into a plasmid vector. The next year, a DNA copy of the RNA genome of poliovirus was produced by reverse transcription and inserted into a plasmid vector. When the cloned copy of the viral genome was introduced into mammalian cells, infectious virus was produced. The infectious viral DNA clone is a double-edged sword. It enables manipulation of the viral genome at will, allowing unprecedented genetic analysis and the use of viruses as vectors for gene therapy. But nearly any virus can now be recovered from the nucleotide sequence – effectively making it impossible to ever truly eradicate a virus from the globe. This was thanks to Baric "reverse genetics."

3. In vitro: The term in vitro refers to a medical study or experiment which is done in the laboratory within the confines of a test tube or laboratory dish. In vivo: The term in vivo refers to a medical test, experiment, or procedure that is done on (or in) a living organism, such as a laboratory animal or human.

DASZAK PROPOSED DOING EXPERIMENTS WITH BAT VIRUSES THAT COULD CAUSE A PANDEMIC: BUT DARPA REFUSED FUNDING BECAUSE:

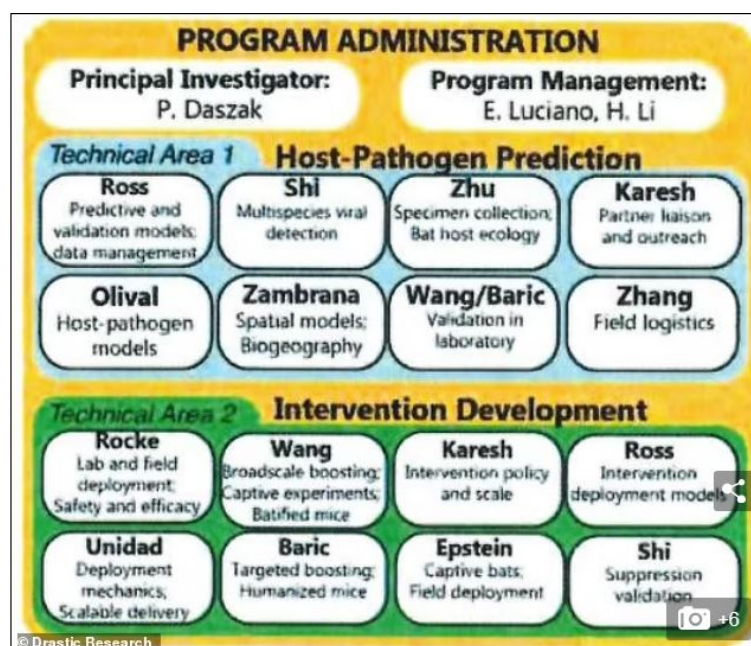
1. The proposal is considered to potentially involve GoF/DURC research because they propose to synthesize spike glycoproteins which bind to human cell receptors and insert them into SARSr-CoV backbones to assess whether they can cause SARS-like disease.

2. However the proposal does not mention or assess potential risks of Gain of Function (GoF) research.

3. Nor does the proposal mention or assess Dual Use Research of Concern (DURC) issues, and thus fails to present a DURC risk mitigation plan.

4. The proposal hardly addresses or discusses ethical, legal, and social issues (ELSI).

[Atlantic Mag. confirms docs authenticity, but claims it does not bolster the lab leak theory.](#) "The most alarming aspect of the research plan revealed in the documents is a plan to search viral genetic databases for new types of 'furin cleavage sites' which help a virus attack a host. According to the proposal, 'high-risk' versions of these sites, once identified, would then be grafted onto SARS-like bat coronaviruses via genetic engineering. [DAILY MAIL](#)....[Lancet Panel Disbanded thanks to Daszak](#)...



HR001118S0017 EcoHealth Alliance (Daszak)

Project DEFUSE

Section II A. EXECUTIVE SUMMARY

Technical Approach: Our goal is to defuse the potential for spillover of novel bat-origin high-zoonotic risk SARS-related coronaviruses in Asia. In **TA1** we will intensively sample bats at our field sites where we have identified high spillover risk SARSr-CoVs. We will sequence their spike proteins, reverse engineer them to conduct binding assays, and insert them into bat SARSr-CoV (WIV1, SHC014) backbones (these use bat-SARSr-CoV backbones, not SARS-CoV, and are exempt from dual-use and gain of function concerns) to infect humanized mice and assess capacity to cause SARS-like disease. Our modeling team will use these data to build **machine-learning genotype-phenotype models** of viral evolution and spillover risk. We will uniquely validate these with serology from previously-collected human samples via LIPS assays that assess which spike proteins allow spillover into people. We will build **host-pathogen spatial models** to predict the bat species composition of caves across Southeast Asia, parameterized

with a full inventory of host-virus distribution at our field test sites, three caves in Yunnan Province, China, and a series of unique global datasets on bat host-viral relationships. By the end of Y1, we will create a prototype app for the warfighter that identifies the "killhood" of a given bat host-viral pathogen at any site across Asia.

What is SARSr-CoV that is being used to circumvent gain-of-function concerns? "Herein, we report the findings of our 5-year surveillance of SARSr-CoVs in a cave inhabited by multiple species of horseshoe bats in Yunnan Province, China. The full-length genomes of 11 newly discovered SARSr-CoV strains, together with our previous findings, reveals that the SARSr-CoVs circulating in this single location are highly diverse in the S gene, ORF3 and ORF8. Importantly, strains with high genetic similarity to SARS-CoV in the hypervariable N-terminal domain (NTD) and receptor-binding domain (RBD) of the S1 gene, the ORF3 and ORF8 region, respectively, were all discovered in this cave. In addition, we report the first discovery of bat SARSr-CoVs highly similar to human SARS-CoV in ORF3b and in the split ORF8a and 8b."

READ THE DOCUMENTS

[DRASTIC Summary of EcoHealth's DEFUSE Grant Proposal](#)

[EcoHealth Alliance Executive Summary of DEFUSE](#)

[EcoHealth's full DEFUSE grant proposal to DARPA](#)

[US Marine Corps Major Joseph Murphy's Analysis Report to Inspector General of DOD and internal Marine Corps email CONTAINS DISFORMATION](#)

"Because Of its (now) known nature, the SARSr-CoV-WIV 's illness is readily resolved with early treatment that inhibits the viral replication that spreads the spike protein around the body (which induce a harmful overactive immune response as the body tries to clear the spikes from the ACE-2 receptors.) Many of the early treatment protocols ignored by the authorities because they inhibit viral replication or modulate the immune response to the spike proteins which makes sense within the context of what Ec-Health was creating. Some of these treatment protocols also inhibit the action of the engineered spike protein. For instance Ivermectin (Identified a curative in April 2020) is identified in the proposal as a SARS-Cov inhibitor, as is interferon (Identified May 2020 as a curative.)"

DASZAK WAS DIRECTLY AND INDIRECTLY INVOLVED IN RECOMBINANT EXPERIMENTS



PETER DASZAK AND RALPH BARIC

Most of the recombinant experiences were carried out by Baric and Shi financed by the NIH and Daszak's re-purposing of Eco-Health grants. **NOVEMBER 21, 2019** Daszak tweeted: "We've made great progress with bat SARS-related CoVs, ID'ing 50 novel strains, sequencing Spike Protein genes, ID'ing ones that bind to human cells, using **recombinant viruses**, humanized mice to see SARS-like signs, and showing some don't respond to MAbs, vaccines."

GIVING A SARS-LIKE VIRUS THE ABILITY TO INFECT HUMANS INVOLVED RECOMBINANT BAT CORONAVIRUSES / NOVEMBER 30, 2017:"DISCOVERY OF A RICH GENE POOL OF BAT SARS-RELATED CORONAVIRUSES PROVIDES NEW INSIGHTS INTO THE ORIGIN OF SARS CORONAVIRUS"

Using the reverse genetics technique we previously developed for WIV1, we constructed a group of infectious bacterial artificial chromosome (BAC) clones with the backbone of WIV1 and **variants** of S genes from 8 different bat SARSr-CoVs. [Ben Hu ,Lei-Ping Zeng , Xing-Lou Yang ,

MANY OF THESE GoF / GoT EXPERIMENTS WERE CONDUCTED WITH VIRUSES FOUND IN HORSESHOE BATS - CLOSE RELATIVES TO THE SARS-CoV-19 VIRUS



Yuan KY et. al. assayed 13 different species of bats. The results proved that **SARS-CoV in bats was the most closely related to that in humans**. The SARS-like CoV in Chinese horseshoe bats has 88%-92% sequence homology with human SARS-CoV. Moreover, the S2 motif in its 3'UTRs and the phylogenetic analyses of four fully characterized genomes of SARS-like CoV indicated that the horseshoe bats have great potential to be one of the natural reservoirs.

<https://onlinelibrary.wiley.com/doi/full/10.1002/ame2.12017>

In **MAY 2016** the United States Government issued a **REPORT** that contained a set of strict rules for determining which DURC GoF/GoT experiments should be funded by the National Institute of Health and other relevant USG entities based on Risk v. Benefit. There was a controversy in the scientific community as to the value of these experiments, however, Daszak was fully committed to performing these procedures and continued to outsource them to the WIV where no such oversight existed.

THE BAT VIRUS STORAGE AND EXPERIMENTS WERE CONDUCTED IN BSL-2 CONSTRUCTED IN 1956 THE ELVIS ERA

Founded in 1956, Wuhan Institute of Virology (WIV), Chinese Academy of Sciences (CAS), was initially named as Wuhan Microbiology Laboratory. It was among the earliest national institutions established after the founding of the New China. In 1961, it became the South China Institute of Microbiology of CAS, and was redesignated as Wuhan Microbiology Institute CAS in 1962. In 1970, under the administration of the Hubei Commission of Science & Technology, it was renamed as Microbiology Institute of Hubei Province. In June 1978, it was returned to the administration of CAS, and adopted its current designation.

BEFORE THE CORONA VIRUS OUTBREAK IN 2019 THE GAIN-OF-FUNCTION, GAIN-OF-THREAT EXPERIMENTS WERE PERFORMED IN BSL-2 LAB

Q: Given that coronavirus research in most places is done in BSL-2 or BSL-3 labs--and indeed, you WIV didn't even have an operational BSL-4 until recently--why would you do any coronavirus experiments under BSL-4 conditions?

A: The coronavirus research in our laboratory is conducted in BSL-2 or BSL-3 laboratories.

After the BSL-4 laboratory in our institute has been put into operation, in accordance with the management regulations of BSL-4 laboratory, we have trained the scientific researchers in the BSL-4 laboratory using the low-pathogenic coronaviruses as model viruses, which aims to prepare for conducting the experimental activities of highly pathogenic microorganisms.

After the COVID-19 outbreak, our country has stipulated that the cultivation and the animal infection experiments of SARS-CoV-2 should be carried out in BSL-3 laboratory or above. Since the BSL-3 laboratories in our institute do not have the hardware conditions to conduct experiments on non-human primates, and in order to carry out the mentioned research, our institute had applied to the governmental authorities and obtained the qualification to conduct experiments on SARS-CoV-2 for Wuhan P4 laboratory, in which the rhesus monkey animal model, etc. have been carried out.

The experimental activities are supervised by our institute's biosafety committee and complied with the biosafety regulations.

For the Shi Zheng Li complete Question and Answer document where she admits to this click **HERE**

"Wuhan Institute of Virology, Wuhan, China (Zhengli Shi and Xingyi Ge) The Shi laboratory includes 4 rooms totaling (b) (4), one equipped with two CO2 incubators for tissue culture, one equipped facilities including with high speed centrifuge, 2 -20°C, 3 -80°C freezers, 2 PCR machines, 1 ELISA plate reader, one for molecule diagnosis equipped with two biosafety cabinets, and one normal laboratory equipped various small equipment items (mini-centrifuges, gel electrophoresis units, circulating adjustable water baths, and heat blocks). Also available to Dr. Shi's group is a fully equipped biosafety level 3 laboratory, a newly opened BSL-4 laboratory (the first in China) and Institute-supported facility center, which houses full-time staff and equipment for electronic microscopy, ultracentrifugation, confocal microscopy, and sequencing machine.

Experiment conducted in BSL-2 Lab

"Everything is assessed on a case-by-case basis." Studies of SARS-CoV-1 and SARS-CoV-2, for instance, have to be done in BSL-3 labs, whereas the human coronaviruses that cause the common cold are handled under BSL-2 conditions. What about bat viruses? The Wuhan institute's biosafety committees ruled a decade ago that while work with animals must be carried out in BSL-3, molecular and cell-culture work involving bat coronaviruses can be done in BSL-2, albeit in biosafety cabinets with air filtration and under negative pressure to keep viruses inside. Dr. Richard Ebright regards this as unsafe. Bat coronaviruses are, as he puts it, "uncharacterized agents" with unknown virulence and transmissibility. "The only acceptable approach is to start with a high biosafety-level assignment ... and to lower the biosafety-level assignment only if and when it is determined it is prudent to do so," he told me in an email."

CHAPTER 3

THE VIRUS IS NOT FROM MOTHER NATURE: THE FBI CORROBORATES THE LAB LEAK THEORY

The FBI is the one agency whose views were identified in the [Biden Report](#) and it stated there was an accidental leak. Yet Carl Zimmer of the NYT continues to put one computer scientist's theory that the virus came from nature on the front page. Daszak is the number one proponent of the "it came from nature" theory to protect himself. After all, how could it be co-incidence that of all the places to first break-out, it was in the same city Daszak's experiments were being conducted on Corona viruses? [*WSJ on the Lab Leak theory*](#)

[The FBI] assesses with moderate confidence that the first human infection with SARS-CoV-2 most likely was the result of a laboratory-associated incident, probably involving experimentation, animal handling, or sampling by the Wuhan Institute of Virology. These analysts give weight to the inherently risky nature of work on coronaviruses...For these hypotheses, IC analysts consider an exposure that occurs during animal sampling activity that supports biological research to be a laboratory-associated incident and not natural contact....They also see the potential that a laboratory worker inadvertently was infected while collecting unknown animal specimens...[The FBI] assesses with moderate confidence that COVID-19 most likely resulted from a laboratory-associated incident involving WIV or other researchers—either through exposure to the virus during experiments or through sampling. Some analysts at elements that are unable to coalesce around either explanation also assess a laboratory origin with low confidence. These analysts place emphasis on academic articles authored by WIV employees indicating that WIV scientists conducted research on other coronaviruses under what these analysts consider to be inadequate biosafety conditions that could have led to opportunities for a laboratory-associated incident. These analysts also take into account SARS-CoV-2's genetic epidemiology and that the initial recorded COVID-19 clusters occurred only in Wuhan—and that WIV researchers who conducted sampling activity throughout China provided a node for the virus to enter the city....[The FBI] finds the laboratory-associated origin theory most likely assess that WIV researchers' inherently risky work with coronaviruses provided numerous opportunities for them to unwittingly become infected with SARS-CoV-2. Although the IC has no indications that WIV research involved SARS-CoV-2 or a close progenitor virus, [the FBI] notes that it is plausible that researchers may have unwittingly exposed themselves to the virus without sequencing it during experiments or sampling activities, possibly resulting in asymptomatic or mild infection. Academic literature indicates that WIV researchers conducted research with bat coronaviruses or collected samples from species that are known to carry close relatives of SARS-CoV-2. Based on currently available information, the closest known relatives to SARS-CoV-2 in bats have been identified in Yunnan Province, and researchers bringing samples to laboratories provide a plausible link between these habitats and the city. [The FBI] analysts that assess COVID-19 most likely originated from a laboratory-associated incident also place emphasis on information suggesting researchers in China used biosafety practices that increased the risk of exposure to viruses. Academic publications suggest that WIV researchers did not use adequate biosafety precautions at least some of the time, increasing the risk of a laboratory-associated incident.

[The FBI] analysts that find the laboratory-associated origin theory most likely assess that WIV researchers' inherently risky work with coronaviruses provided numerous opportunities for them to unwittingly become infected with SARS-CoV-2. Although the IC has no indication that WIV research involved SARS-CoV-2 or a close progenitor virus, [the FBI] analysts note that it is plausible that researchers may have unwittingly exposed themselves to the virus without sequencing it during experiments or sampling activities, possibly resulting in asymptomatic or mild infection. Academic literature indicates that WIV researchers conducted research with bat coronaviruses or collected samples from species that are known to carry close relatives of SARS-CoV-2.

- Based on currently available information, the closest known relatives to SARS-CoV-2 in bats have been identified in Yunnan Province, and researchers bringing samples to laboratories provide a plausible link between these habitats and the city.

- [The FBI] analysts also note that China's investigations into the pandemic's origin might not uncover evidence of a laboratory-associated incident if it involved only a small number of researchers who did not acknowledge or have knowledge of a potential infection. [FBI IC VIEWS REVEALED](#)

FORMER FDA HEAD SCOTT GOTTLIEB ALSO MAKES THE CASE FOR THE LAB LEAK THEORY



Q "What did you learn in the course of your research about the origins of COVID?

A. I learned that we're not going to answer this question absent one of two things happening, **either we find the intermediate host, the animal that spread COVID, or there's a whistleblower inside China**, or someone close to this who knows that this came out of a lab, comes forward, defects, goes overseas, or we intercept some communication that we shouldn't have had access to. Absent something like that, we're not going to be able to answer this question. This is going to be a battle of competing narratives. I think over time, the side of the ledger that that says that this might have come out of a lab has grown more robust and the side of the ledger that this came out of a natural species has not really moved. And if anything, you can argue that side of the ledger has been diminished by a couple of facts. Number one, we've looked for the intermediate host and we haven't found it. And number two, the idea that the market, this initial market, was the source of the initial spread has been firmly debunked, even the Chinese acknowledged that. And that was a big part of the thesis around the zoonotic origin, the animal origin, because the idea was that the animal was in that market. We now know that market wasn't the source of the spread. It was a path along the spread. Beijing has even acknowledged that-- Beijing had acknowledged it, right.

Q. But when you say intermediate host, you mean what happened between the bat and the human, who came in between.

A. There's an animal, maybe a pangolin, there's some other animal in between and it could have been-- it wasn't necessarily a bat and it could have been a bat to a human, **but we haven't found the virus in nature**. And there's been a pretty exhaustive search. The Chinese have mounted an exhaustive search, and I don't think that the fact that they've been looking for it proves that they know it didn't come out of a lab. I think that they would be looking for it even if they knew it came out of a lab. And the reality is if it came out of a lab, the number of people who actually are aware of that could be a very small subset of people.

Q. When you say came out of a lab, you were saying through a lab accident, not a construct?

A. Yeah. No, I don't think anyone, and the administration has said this in the intelligence report they put out that they don't believe-- they've sort of firmly debunked the idea that this was something that could have deliberately come out of a lab, or was deliberately engineered. But the possibility is that you've had labs doing research on novel coronaviruses, you had novel coronaviruses being brought to those labs, particularly the Wuhan Institute of Virology. **We know that they were doing that research in what's called BSL-2 labs, lower security labs, where tight precautions aren't taken. We also know that the Wuhan Institute of Virology [BSL-4] was a sloppy lab.** At the time that it opened, there was an article in the journal *Science* raising questions about the integrity of that lab where scientists at the time that it opened in 2017 [2018] said, we're worried about the procedures in this lab. We're worried about the training, we're worried about the way it was built. We know that the lab was conducting high-end research with the Chinese military. The French were in that lab and were eventually kicked out. And at the time that they were kicked out, they were aware that the Chinese military had moved into that lab. So there were circumstances created around that facility, and there were operating procedures around that facility that created a lot of risk. That doesn't mean it came out of the lab, but it certainly makes that a suspect location. And there was another lab. The CDC, the Chinese CDC maintained a lab literally blocks from the wet market that was first implicated in this virus that was also conducting coronavirus research in BSL-2 labs.

Q. So other than the whodunit factor, why does it matter? Why do we need to know who patient 0 is? And how will that affect the Biden administration's response?

A. Yeah, it matters a lot because if we determine-- first of all, if we determine that this came out of a lab or we even assess that there's a high probability that this came out of a lab, I think it changes how we try to govern research internationally. We're going to need something like the International Atomic Energy Agency for BSL 4 labs. We're going to have to look much more carefully about who's creating BSL 4 labs, the kind of research going on in those labs.

Q. On the global response, you wrote, COVID crushed the global order of public health cooperation. Are you saying WHO is just not up to the task?

A. Well, it's not just the WHO. I mean, past epidemics crushed the global order of cooperation. We just didn't learn the lesson.

Q. Was there quashing of information by the WHO?

A. I think the WHO, for too long--

Q. Did they cover up for China, is the allegation.

A. They weren't willing to confront China, right? They put out statements extolling China's behavior and how forthcoming China was. I mean, it's part of the record now. Tedros, it's in his Twitter feed, it's in the Twitter feed of the head of the WHO giving props to China for how forthcoming they were. Now, was some of that an attempt to try to give them public praise because privately you were giving them a harder sell? I think some of that was going on in the US with some of the tweets and the statements that we were putting out. I don't know that that was happening at the WHO level because I was talking to some WHO officials at the time and have talked to a number since. And I think the WHO really did believe China was behaving in sort of an appropriate way and was providing cover for them as they were getting criticized by other parts of the world. Clearly, they weren't. And I think that that was knowable at the time. I mean, China didn't share the source strains. Tedros of WHO didn't want to push China on sharing the source strains publicly because he said, well, they have no commitment to do it. And he's right. Under the International Health Regulations, there was no requirement that you had to share the samples. But there were requirements that you had to share samples of novel emerging respiratory pathogens and other settings. So clearly, the spirit of the International Health Regulations was that this should be shared. But because it wasn't the letter of the law, the WHO didn't want to push China publicly to do it, even though that would have been very helpful for other countries.

Q. You're talking about actual viral samples not the sequence--

A. Right. Actual samples of the virus because the sequence alone isn't good enough if you want to develop a vaccine or a diagnostic. You actually at some point need the live virus. Now, we eventually got the live virus because we had spread here in the United States but, you know, at least publicly we didn't have the virus until there was a case in Seattle. It's possible we got the virus earlier from one of China's neighbors where there was some earlier spread.

Q. That part of the equation being dealt with now?

A. No, I don't think the WHO has taken any steps to reform how it operates in a global crisis like this. Whether or not they're able to-- whether or not the organization has a self-awareness to do that and is able to self-organize to actually implement meaningful reform, I'm not sure. I think the Biden administration lost an opportunity to compel different behavior at the WHO by simply rejoining the WHO. I was critical at the time that President Trump made the decision to pull out of the WHO, I had actually spoken with him directly, urging him not to do it, suggested that there were other ways he could send a strong message to China short of pulling out of the WHO. But once we pulled out of the WHO, and we were going to re-enter, we should have used the reentry to extract some kind of agreement about the WHO engaging in some reform process. And as best I know, and as best we all know based on what's public, that wasn't done. The leverage was given up.

CHAPTER 4

FAUCI, NIH, STEMMY, DASZAK, COLLINS DOCUMENTS AND INVOLVEMENT IN THE PANDEMIC

SEARCHABLE NIH / NIAID DOCS SEARCHABLE NIH / NIAID DOCS 2

FAUCI IS A PROPONENT OF THE ANIMAL SPILL OVER THEORY BECAUSE THE LAB LEAK ONE LEADS BACK TO HIM

A group of virologists, many of whom receive funding from Fauci's NIH, or as we say in the vernacular, were on Fauci's pad, wrote: "The suspicion that SARS-CoV-2 might have a laboratory origin stems from the *coincidence* that it was first detected in a city that houses a major virological laboratory that studies coronaviruses." **They claim it started in the Wet Market there. A large city in China typically has a few hundred wet markets.** Why this particular one near the WIV? If the disease came from rural China, as Daszak suggests, why didn't anyone get infected along the way? But because Trump the Hump said the pandemic was caused by a lab leak, it became a partisan issue.

FRANCIS COLLINS RESIGNS





Claims it has nothing to do with his approval of Daszak's experiments! Ha! Ha! The Human Genome Project, which James Watson helped initiate in 1988, assembled a composite 'reference' genome of DNA from many individuals. Francis Collins was NIH director part of the time the study was conducted and did not participate in the actual research. Watson, who discovered DNA's double helix structure alongside Francis Crick and Rosalind Franklin in the 1950s, said that genes cause a difference on IQ tests between blacks and whites. African-Americans represent just 1.5 percent of grant applications to the N.I.H. which Collins headed, but none of these grant applications involved Gain-of-Threat research, so what race are stupid, evil ones from? Scientists and public health experts have criticized [Collins'] efforts at studying Covid-19 treatments, saying some that ultimately did not show strong results — such as convalescent plasma and hydroxychloroquine — were prioritized over more rigorous research. [NYT](#)

INVOLVEMENT IN THE PANDEMIC

BENEFITS AND RISKS OF INFLUENZA RESEARCH: LESSONS LEARNED ANTHONY S. FAUCI, FRANCIS S. COLLINS

THE DOCUMENTS MAKE IT CLEAR THAT ASSERTIONS BY THE NIH DIRECTOR, FRANCIS COLLINS, AND THE NIAID DIRECTOR, ANTHONY FAUCI, THAT THE NIH DID NOT SUPPORT GAIN-OF-FUNCTION RESEARCH OR POTENTIAL PANDEMIC PATHOGEN ENHANCEMENT AT WIV ARE UNTRUTHFUL.

THE US NATIONAL INSTITUTES OF HEALTH (NIH) ANNOUNCED THAT THEY WOULD RESUME FUNDING GAIN-OF-FUNCTION EXPERIMENTS INVOLVING INFLUENZA, MIDDLE EAST RESPIRATORY SYNDROME CORONAVIRUS, AND SEVERE ACUTE RESPIRATORY SYNDROME CORONAVIRUS.

FEDERAL OFFICIALS ENDED A MORATORIUM IMPOSED THREE YEARS AGO ON FUNDING RESEARCH THAT ALTERS GERMS TO MAKE THEM MORE LETHAL

"WE DEBATED UP ONE SIDE DOWN THE OTHER, AND ULTIMATELY DECIDED IF YOU WERE A HUMAN TRYING TO DESIGN A REALLY DANGEROUS CORONAVIRUS, YOU WOULD NOT DESIGN THIS ONE."

EXEMPTION 5 IS COMMONLY INTERPRETED AS SHIELDING FROM RELEASE DRAFT GOVERNMENT DOCUMENTS, RECORDS OF SENSITIVE DELIBERATIONS BEFORE DECISIONS ARE MADE, AND GOVERNMENT ATTORNEY-CLIENT DELIBERATIONS.

FRANK COLLINS CLAIMS NEITHER NIH NOR NIAID HAVE EVER APPROVED ANY GRANT THAT WOULD HAVE SUPPORTED GAIN-OF-THREAT RESEARCH ON CORONAVIRUSES THAT WOULD HAVE INCREASED THEIR TRANSMISSIBILITY OR LETHALITY FOR HUMANS MORONICAL MD FRANCIS "THE SINGING MULE" COLLINS CHANGES SONG ABOUT SMOKING OPIUM AS IN "CHASING THE DRAGON" INTO SONG ABOUT COVID

ON SANJAY GUPTA'S CNN ORIGINS OF COVID DASZAK SAID IN THE VENACULAR: "FAUCI HE BE MY HOMEBOY"



Here is our president Dr. Peter Daszak teaching CNN's Dr. Sanjay Gupta the "Wuhan shake": a safer way to greet each other without physical

contact.

Please check out CNN's new podcast on [#COVID19](https://www.cnn.com/audio/podcasts/corona-virus) to hear their chat about how we can prevent pandemics.

<https://www.cnn.com/audio/podcasts/corona-virus>

46 5 18

GUPTA: These exchanges seem to assert that U.S. taxpayer dollars, via the NIH through your organization went to the Wuhan Institute of Virology and funded gain of function research.

DASZAK: Yes.

GUPTA: Which may, not definitively by any means, but may have been a source of this pandemic. What do you say?

DASZAK: That's just plain not true. **Dr. Fauci testified publicly under oath that that's not true and he's right. We didn't do work that run against any of the rules.**

[Gupta / Daszak Transcript](#)

Daszak knew they were being conducted in a leaky BSL-2 lab because he had been there many times in person. Was Daszak just negligent, or is there something sinister going on here? The answer lies in [Entire EcoFascist Manifesto](#) he co-authored along with his close associate Aleksei Chmura.

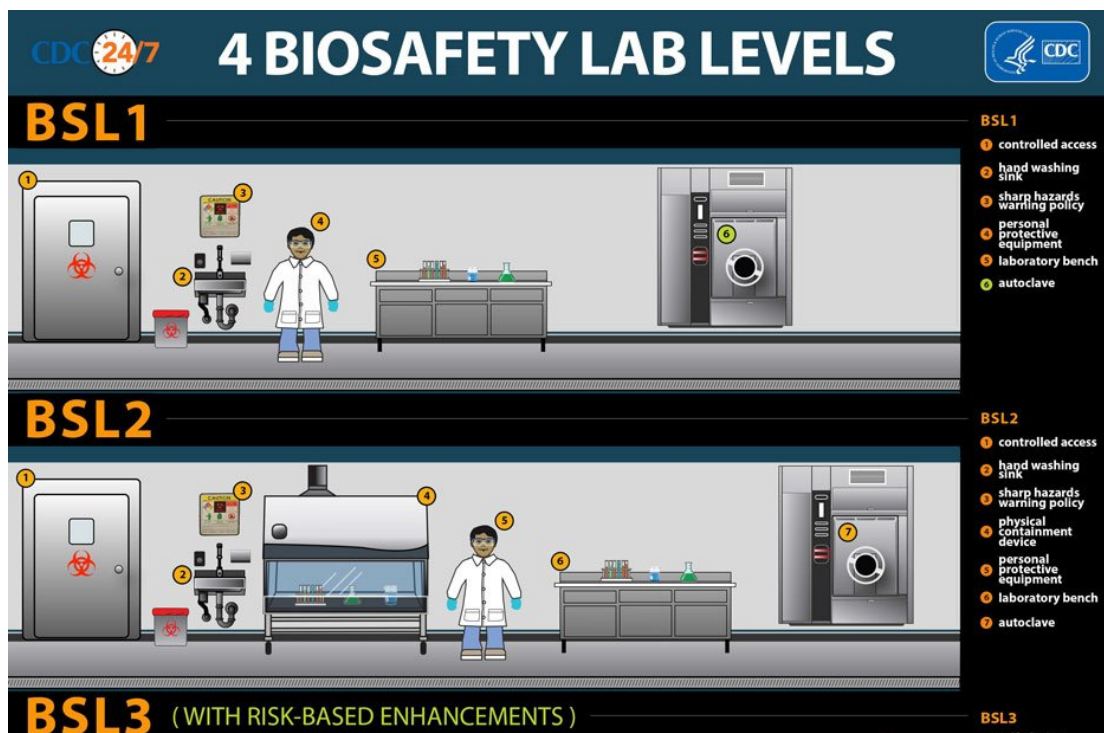
If the fallen angels [\[in the BRUEGEL painting\]](#) represent the evil mirror image of St. Michael and his cohort, so they also represent the mirror image of our own genetic kind—pathogenic organisms which are otherwise just like us, but have fallen from grace through an evolutionary (not spiritual) pathway that takes them to a netherworld where they can feed only on our genes, our cells, our flesh... In Bruegel's curious chimeras, we find yet another analogy—for the genetic recombination, mutation and evolution that negative-stranded RNA viruses in particular undergo as they shift, morph and adapt to their changing habitat—animal cells... Perhaps he reminds us also that it is the nature of our interactions with wildlife—here represented as an evil entity for humanity to vanquish—which cause new zoonoses to emerge in the first place. Perhaps the EcoHealth view is that if we tread carefully, we might avoid those nasty little pincers waiting to nip!

CHAPTER 5

KEY UNWITTING PERSONNEL

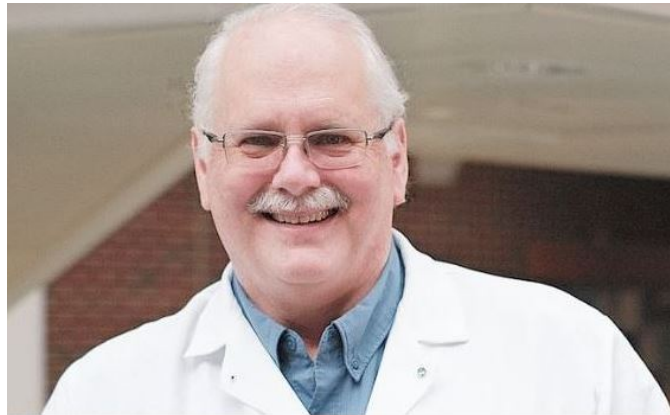
There was no COVID conspiracy: Daszak manipulated several **unwitting key figures** and a SARS virus found in bats was genetically engineered to be a novel Covid virus or a natural virus, that shouldn't have been in the BSL-2 lab, escaped. The original SARS already had caused a minor pandemic: SARS surfaced in the fall of **2002** in Guangdong Province, China. The original SARS-CoV spread worldwide within a few months, though it was quickly contained. SARS-CoV was shown to be transmitted from civet cats to humans. In **2015** Baric and Shi Zheng Li discovered the civets contracted the virus from bats, then authored a **scientific peer-reviewed paper** that stated that virologists better keep a close watch on the bat viruses in China because they were poised to spill over and cause a pandemic. Daszak is not listed in this paper which was credible. The Chinese China built the [BSL-4 the Wuhan Institute of Virology \(WIV\)](#) in 1956 but didn't give them the BSL-4 Lab, the highest bio-security lab, until 2018 because of dual use biowarfare concerns. The BSL-4 Lab is for diseases for which there is no known vaccine, cure or therapeutic. The gain-of-threat experiments should have been conducted there. This aspect brought the [MIT Tech Review](#) to it's senses about "conspiracy theory" being an excuse for a lab leak:

The CDC recognizes four levels of biosafety and recommends which pathogens should be studied at which level. Biosafety level 1 is for nonhazardous organisms and requires virtually no precautions: wear a lab coat and gloves as needed. BSL-2 is for moderately hazardous pathogens that are already endemic in the area, and relatively mild interventions are indicated: close the door, wear eye protection, dispose of waste materials in an autoclave. BSL-3 is where things get serious. It's for pathogens that can cause serious disease through respiratory transmission, such as influenza and SARS, and the associated protocols include multiple barriers to escape. Labs are walled off by two sets of self-closing, locking doors; air is filtered; personnel use full PPE and N95 masks and are under medical surveillance. BSL-4 is for the baddest of the baddies, such as Ebola and Marburg: full moon suits and dedicated air systems are added to the arsenal. "There are no enforceable standards of what you should and shouldn't do. It's up to the individual countries, institutions, and scientists."





Ralph Steven Baric, (born 1954) Daszak's former unwitting accomplice, who believed he was working to develop a vaccine, Dr. Ralph Baric, stated: "The experiments that they did under the conditions that they did them were risky. **They're working on bats SARS like viruses that have never been shown to cause human infection.** Well, there are some scientists speaking up, that can't rule out the possibility of a lab leak. Their papers indicate that they did much of their work with these bat viruses under biological safety two conditions. There are many more laboratory accidents or laboratory acquired infections BSL-2 as compared to BSL-3. We do all the research in our lab on bat related coronaviruses under biological safety three enhanced conditions. We wear portable air breathing apparatuses with tied back suits so the workers are protected from anything that might be in the laboratory."



RALPH BARIC

BARIC: "You can engineer a virus without leaving any trace. The answers you are looking for, however, can only be found in the archives of the Wuhan laboratory."

Baric was able to increase the virulence of viruses by cutting their RNA into strips and altering each individual piece of genetic material. Baric was also known for his senseless experiments such as the creation of "no-see-um" viruses, through passaging¹, that showed no traces of genetic manipulation. This technique, which was taught to Shi Zheng Li thanks to Daszak, was instrumental in making it difficult to determine the lab origin SARS-CoV-19, since virus was passaged to make it infect new hosts in an effort to determine which virus will spillover to humans. Baric also developed a method to bring viruses of the past, such as polio, back, through reverse genetic engineering. So a virus could never be wiped off the planet as long as its nucleic code existed. Nucleic acid is a complex organic substance present in living cells, especially DNA or RNA, whose molecules consist of many nucleotides linked in a long chain. Baric once gave a lecture on how to profit from a pandemic. Baric erred and caused a minor [SARS outbreak in North Carolina 2003. Look at the document.](#) Later, one of his SARS-infected lab rats bit a student's hand. Baric applied for patents for his inventions and had a large staff at the University of North Carolina. Baric visited the WIV and the Bat Lady visited his lab - thanks to Daszak bringing them together. It should be noted that "although GoF experiments can make a virus more deadly and transmittable many gain-of-function experiments were worthwhile. In 1937, researchers found that when they passed the yellow fever virus through chicken cells, it lost the ability to cause disease in humans — a discovery that led to a vaccine for yellow fever." But Baric's creations were often pointless. [Baric's base salary is \\$190,300.00 a year.](#)

At a regular basis, Dr. Baric will report the results of the teams research to Dr. Daszak and Dr. Shi and together, they will use this information to identify additional research priorities and design downstream studies. Ors. Daszak, Shi and Barie have published together in the past and participated on research project applications. Dr. Barie recently spent several days in Wuhan, China, where he discussed research strategies and collaborations with Dr. Daszak and Dr. Shi. He will work closely with Dr. Sims and Mr. Yount to prepare timely reports, share research and discuss future research directions with the group. [Baric Sub-award](#) Baric's base salary is \$190,300.00 a year.

1. Passaging is the placing of a live virus into an animal or cell culture to which it is not adapted and then, before the virus dies out, transferring it to another animal or cell of the same type. Passaging is often done iteratively. The theory is that the virus will rapidly evolve (since viruses have high mutation rates) and become adapted to the new animal or cell type. Passaging a virus, by allowing it to become adapted to its new situation, creates a new pathogen. [SCIMEX](#)

They're working on bats SARS like viruses that have never been shown to cause human infection. This means they are enhancing them to do so - this is known as "Gain-of-Threat." [MIT TECHNOLOGY REVIEW](#) puts a lot of blame on Ralph Baric. However Baric's father was not a Nazi death camp executioner, like Daszak's father Bohdan, who justified his crimes to his son by inculcating him with Nazi ideology. Evil runs in Daszak's blood. Daszak's father, already a Ukrainian Nazi, volunteered to become a death camp executioner.





RALPH BARIC

RALPH BARIC'S ROLE IN CREATING THE PANDEMIC

Ralph Baric, although at least one of his experiments seemed pointless, like developing a method that made it impossible to discern a artificial virus from a natural one, never funneled any of his USG grant money to the WIV like Daszak did but he collaborated with it. Baric did give a lecture titled "How to Profit from the Next Pandemic." Baric was a cowboy and out of control. His lab was known as "The Wild West." His experiments may have caused a minor outbreak of SARS CoV-1 in Chapel Hill, North Carolina in 1983. His experiments must be reviewed to determine if they were a threat to humanity. For 20 years, beneath the radar, Baric had been playing with millions of people's lives. In Wuhan, China and Chapel Hill, North Carolina, Daszak, Dr. Shi Zheng Li collaborated with Dr. Ralph Baric, and routinely created viruses more dangerous than those that exist in nature.

Dr. Baric had developed, and taught Dr. Shi a general method for engineering bat coronaviruses to attack other species. What was worse, Baric had developed a method of genetic engineering wherein it was impossible to determine if the virus had been altered, which he called the "no-see-um" technique after the pesky little, almost invisible, flies found at various beaches in the South. *The point of doing this escapes me?* The specific targets were human cells grown in cultures and humanized mice. These laboratory mice are genetically engineered to carry the human version of a protein called **ACE2** that studs the surface of cells that line the lungs. The "Bat Lady" flew back to her lab at the Wuhan Institute of Virology (**WIV**) and resumed the work she had started on genetically engineering coronaviruses to attack human cells using this technique that she learned from Dr. Baric. Her genetically altered virus, enhanced to attack human beings, escaped. It wasn't the first time a genetically altered SARS virus leaked. **Evidence suggests that in 2003 a less virulent SARS virus escaped from Baric's North Carolina lab causing several infections.**

When you are dealing Baric remember one thing. The University of North Carolina School of Medicine, ranked 17th in the country in total National Institutes of Health (NIH) funding for federal fiscal year 2020 and 5th among peer public universities, according the Blue Ridge Institute for Medical Research. The total dollar amount is \$345,729,473, a jump of more than \$29 million from FY 2019. This amount does not include research and development contracts with the NIH. The UNC Gillings School of Global Public Health, which is part of UNC, where Ralph Baric works, is ranked 3rd in total NIH funding, 1st among public universities. Fauci has been his boss for decades. Baric signed on to the email calling for new Covid-19 investigation and didn't sign Daszak's email supporting the Zoonotic theory to disguise his part in the pandemic.



Baric, a former swim champion, described in this early paper how his lab was able to train a coronavirus, MHV, which causes hepatitis in mice, to jump species, so that it could reliably infect BHK (baby-hamster kidney) cell cultures. They did it using serial passaging: repeatedly dosing a mixed solution of mouse cells and hamster cells with mouse-hepatitis virus, while each time decreasing the number of mouse cells and upping the concentration of hamster cells. At first, predictably, the mouse-hepatitis virus couldn't do much with the hamster cells, which were left almost free of infection, floating in their world of fetal-calf serum. But by the end of the experiment, after dozens of passages through cell cultures, the virus had mutated: It had mastered the trick of parasitizing an unfamiliar rodent. A scourge of mice was transformed into a scourge of hamsters. And there was more: "It is clear that MHV can rapidly alter its species specificity and infect rats and primates," Baric said. "The resulting virus variants are associated with demyelinating diseases in these alternative species." (A demyelinating disease is a disease that damages nerve sheaths.) With steady prodding from laboratory science, along with some rhetorical exaggeration, a lowly mouse ailment was morphed into an emergent threat that might potentially cause nerve damage in primates. That is, nerve damage in us. A few years later, in a further round of "interspecies transfer" experimentation, Baric's scientists introduced their mouse coronavirus into flasks that held a suspension of African-green-monkey cells, human cells, and pig-testicle cells.

2002 Dr. Baric announced that he found a way to create a **full-length infectious clone of the entire mouse-hepatitis genome. His "infectious construct" replicated itself just like the real thing, he wrote. Not only that, but he'd figured out how to perform their assembly seamlessly, without any signs of human handiwork. Nobody would know if the virus had been fabricated in a laboratory or grown in nature.** Baric called this the "*no-see'm method*," and he asserted that it had "broad and largely unappreciated molecular biology applications."

<https://nymag.com/intelligencer/article/coronavirus-lab-escape-theory.html>

BARIC WAS CONDUCTING SARS RESEARCH BEFORE A 2003 OUTBREAK IN CHAPEL HILL NORTH CAROLINA



RALPH BARIC

A. Professional Development/Invited Presentations

Invited Speaker: **Engineering the Genomes of Microorganisms**. DARPA Meeting on "Synthetic Biology," Menlo Park, California. **March 2003**.

Invited Speaker: **Coronavirus Vaccines**. NIAID. SARS: Developing a Research Response, **May 30, 2003**

Coronavirus Reverse Genetics. Layola University School of Medicine, **March 2003**.

Grant Review **2003**

1. Genetics study section **FEBRUARY and OCTOBER, 2003**. Ad hoc.

2. Experimental Virology, **FEBRUARY, 2003**. Ad hoc

3. NIH ad hoc review, Poxvirus vaccine program project. **SEPTEMBER 2003**.

<https://media-speakerfile-pre.s3.amazonaws.com/documents/cc4e5e5d442320c20c7f76a0c3cadce51445358867.pdf>

BARIC'S LAB LEAKED IN 2003 AND CAUSED A MINOR EPIDEMIC IN NORTH CAROLINA

The Baric laboratory has pioneered reverse genetic analyses of CoVs and DENVs. Several CoV infectious cDNA clones are available in the lab, including SARS-CoV, MERS-CoV, conventional human and model CoVs, and several bat Co Vs with pandemic potential. The availability of these genetic platforms allows for detailed studies into the role of viral genes in pathogenesis, innate immune antiviral immunity, vaccine performance and design, virus-receptor interactions, entry and virus evolution.

Baric Bio Intercept

The CDC reported: **"DECEMBER 31, 2003** In the United States, EIGHT SARS infections were documented by laboratory testing and an additional 19 probable SARS infections were reported.

<https://www.cdc.gov/about/history/sars/timeline.htm>

The North Carolina Department of Health and Human Services (DHHS) **March 19, 2003**: Two possible SARS cases reported in N.C., one in WAKE COUNTY [where Baric's UNC lab is located] and one in ORANGE COUNTY. Both cases subsequently tested negative. **April 1, 2003**: Third and fourth cases of suspected SARS reported, (one in WAKE COUNTY and one in Mecklenburg County). Both cases subsequently tested negative. **April 8, 2003**: Fifth case of suspected SARS reported (Iredell County). Case subsequently tested negative. **April 9, 2003**: Sixth suspected SARS case reported (WAKE COUNTY). Case subsequently tested negative. **April 21, 2003**: Seventh suspected SARS case reported (WAKE COUNTY). Case subsequently tested negative. **April 28, 2003**: EIGHTH suspected SARS case (WAKE COUNTY). Case tested negative. **June 3, 2003**: North Carolina reported its ninth case of suspected SARS, an ORANGE COUNTY man, to the Centers for Disease Control and Prevention (CDC). He was reported as probable on **June 6, 2003**, and then as a confirmed case of SARS on **June 9, 2003**, when CDC laboratory tests were positive. By the time North Carolina reported its confirmed case in **June 2003**, that case was the eighth laboratory-confirmed case of SARS in the United States. No further confirmed cases were reported in the U.S., and the transmission of SARS-CoV was declared contained in July 2003.

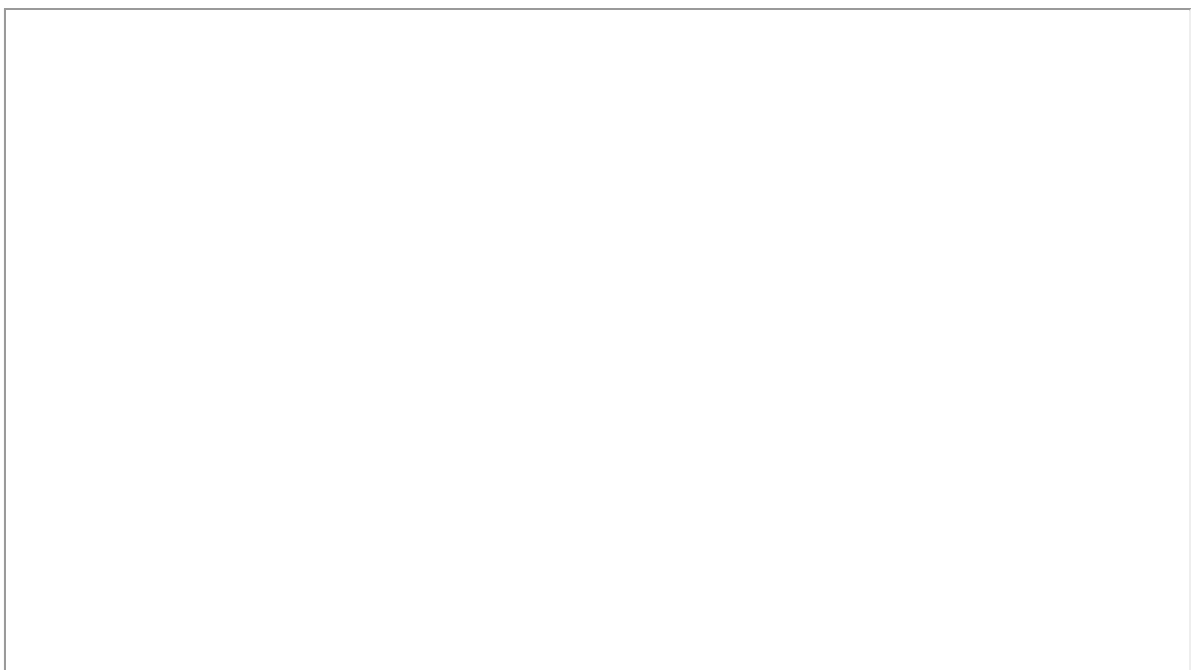
<https://epi.dph.ncdhhs.gov/cd/sars/SARSinNorthCarolina2003.pdf>

HOW CAN YOU HAVE SARS-RELATED SYMPTOMS AND NOT HAVE SARS?

"THE EIGHT PREVIOUSLY REPORTED SUSPECTED SARS CASES HAVE ALL RECOVERED FROM THEIR SARS-RELATED SYMPTOMS"

APRIL 28, 2003: "North Carolina has reported its EIGHTH case of suspected SARS to the Centers for Disease Control and Prevention. The patient is a WAKE COUNTY woman who developed a fever and respiratory symptoms after returning to WAKE COUNTY from a trip to TORONTO, CANADA. The patient is recovering and is under voluntary isolation at home. **THE OTHER SEVEN SUSPECTED CASES OF SARS IN NORTH CAROLINA HAVE ALL NOW RECOVERED FROM THEIR SARS-RELATED SYMPTOMS** and may return to their normal activities. **June 3, 2003**: North Carolina reported its ninth case of suspected SARS to the Centers for Disease Control and Prevention (CDC). The patient is an ORANGE COUNTY man who developed symptoms after returning to North Carolina from a trip to TORONTO, CANADA. He is being treated as an outpatient and is recovering at home under isolation.

<https://epi.dph.ncdhhs.gov/cd/sars/SARSinNorthCarolina2003.pdf>



SARS-CoV infected around 8000 individuals worldwide with an overall mortality of 10% during the 2002–2003 pandemic. Two of the North Carolina cases came from the Toronto outbreak caused by a woman who returned from Hong Kong but what about the others? As of May 7, 2003 a total of 328 SARS cases in the United States were reported from 38 states, of which 265 (81%) were classified as suspect SARS, and 63 (19%) were classified as probable SARS (more severe illnesses). There seems to be a disproportionate number of cases in North Carolina but due to medical privacy concerns we will never know if they were in or around Chapel Hill? (one case was reported there)

<https://www.cdc.gov/mmwr/preview/mmwrhtml/mm5218a2.htm>

Also see: https://www.washingtonpost.com/opinions/a-flu-virus-risk-worth-taking/2011/12/30/gIQA9sNRP_story.html



RALPH S. BARIC AND SHI ZHENGLI BEGAN COLLABORATING IN 2015

GAIN OF FUNCTION / GAIN-OF-THREAT RESEARCH INVOLVES CREATION OF RECOMINANT VIRUS IN UNIVERSITY OF NORTH CAROLINA IN COLLABORATION WITH SCIENTISTS FROM WIV

NOVEMBER 2015 "Utilizing the SARS-CoV infectious clone, we generated and characterized a chimeric virus expressing the spike of bat coronavirus SHC014 in a mouse adapted SARS-CoV backbone. The results indicate that group 2b viruses encoding the SHC014 spike in a wild type backbone can efficiently utilize multiple ACE2 receptor orthologs¹, replicate efficiently in primary human airway cells, and achieve in vitro titers² equivalent to epidemic strains of SARS-CoV. Additionally, in vivo experiments demonstrate replication of the chimeric virus in mouse lung with notable pathogenesis. Evaluation of available SARS-based immune-therapeutic and prophylactic modalities revealed poor efficacy; both monoclonal antibody and vaccine approaches failed to neutralize and protect from CoVs utilizing the novel spike protein. Importantly, based on these findings, we synthetically rederived an infectious full length SHC014 recombinant virus and demonstrate robust viral replication both in vitro and in vivo. Together, the work highlights a continued risk of SARS-CoV reemergence from viruses currently circulating in bat populations."....While offering preparation against future emerging viruses, this approach must be considered in the context of the US government-mandated pause on GoF/GoT studies. Based on previous models of emergence the creation of chimeric viruses like SHC014-MA15 was not expected to increase pathogenicity. However, while SHC014-MA15 is attenuated relative to parental mouse adapted, equivalent studies examining the wild-type Urbani spike within the MA15 backbone produced no weight loss and replication attenuation. As such, relative to the Urbani Spike-MA15 CoV, SHC014 MA15 constitutes a gain in pathogenesis. Based on these findings, review panels may deem similar studies too risky to pursue as increased pathogenicity in mammalian models cannot be excluded. Coupled with restrictions on mouse adapted strains and monoclonal antibodies generated against escape mutants, research into CoV emergence and therapeutic efficacy may be severely limited moving forward. Together, these data and restrictions represent a crossroads of GoF/GoT research concerns; the potential to prepare and mitigate future outbreaks must be weighed against the risk of creating more dangerous pathogens. In developing policies moving forward, it is important to consider the value of the data generated by these studies and if they warrant further study or the inherent risks involved.

1. Orthologs are genes in different species that evolved from a common ancestral gene by speciation, and, in general, orthologs retain the same function during the course of evolution.

2. The concentration of an antibody, as determined by finding the highest dilution at which it is still able to cause agglutination (the clumping together in suspension of antigen-bearing cells in the presence of specific antibodies of the antigen).

Reported studies were initiated after the University of North Carolina Institutional Biosafety Committee approved the experimental protocol: **PROJECT TITLE: GENERATING INFECTIOUS CLONES OF BAT SARS-LIKE COVS; LAB SAFETY PLAN ID: 20145741; SCHEDULE G ID: 12279.** These studies were initiated prior to the U.S. Government Deliberative Process Research Funding Pause on Selected GoF/GoT Research Involving Influenza, MERS, and SARS Viruses and the current manuscript has been reviewed by the funding agency, the National Institutes of Health (NIH). **Continuation of these studies have been requested and approved by NIH. [Fauci]**

FULL STORY "Researchers from the University of North Carolina at Chapel Hill have discovered a new bat SARS-like virus that can jump directly from its bat hosts to humans without mutation. However, researchers point out that if the SARS-like virus did jump, it is still unclear whether it could spread from human to human. The discovery, reported in the November 9, 2015 issue of *Nature Medicine*, is notable not only because there is no treatment for this newly discovered virus, but also because it highlights an ongoing debate over the government's decision to suspend all gain-of-function experiments on a variety of select agents earlier this year. The move has put a substantial standstill on the development of vaccines or treatments for these pathogens should there be an outbreak. "Studies have predicted the existence of nearly 5,000 coronaviruses in bat populations and some of these have the potential to emerge as human pathogens," said senior author **Ralph Baric**, a faculty member at the Gillings School of Global Public Health and expert in coronaviruses. "So this is not a situation of *if* there will be an outbreak of one of these coronaviruses but rather when and how prepared we'll be to address it." SARS first jumped from animals to humans in 2002-2003 and caused a worldwide outbreak, resulting in 8,000 cases, **including one case in Chapel Hill**. With nearly 800 deaths during that outbreak, SARS-CoV presents much like flu symptoms but then can accelerate, compromise breathing and bring on a deadly form of pneumonia. The outbreak was controlled through public health interventions and the original virus was thought to have been extinct since 2004. Baric and his team demonstrated that the newly-identified SARS-like virus, labeled **SHC014-CoV** and found in the Chinese horseshoe bats, can jump between bats and humans by showing that the virus can latch onto and use the same human and bat receptor for entry. **[ACE2]** The virus also replicates as well as SARS-CoV in primary human lung cells, the preferred target for infection. "This virus is highly pathogenic and treatments developed against the original SARS virus in 2002 and the ZMapp drugs used to fight Ebola fail to neutralize and control this particular virus," said Baric. "So building resources, rather than limiting them, to both examine animal populations for new threats and develop therapeutics is key for limiting future outbreaks." Journal Reference: Vineet D Menachery, Boyd L Yount, Kari Debbink, Sudhakar Agnihothram, Lisa E Gralinski, Jessica A Plante, Rachel L Graham, Trevor Scobey, Xing-Yi Ge, Eric F Donaldson, Scott H Randell, Antonio Lanzavecchia, Wayne A Marasco, **SHI ZHENGLI-LI** Ralph S Baric. A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence. *Nature Medicine*, 2015; DOI: 10.1038/nm.3985

BARIC'S LAB RAT BITES STUDENT

by Jonathan Latham, PhD

University researchers genetically engineer a human pandemic virus. They inject the new virus into a laboratory mouse. The infected mouse then bites a researcher.It is a plot worthy of a Hollywood blockbuster about risky coronavirus research. But according to newly obtained minutes of the Institutional Biosafety Committee (IBC) of the University of North Carolina (UNC), Chapel Hill, these exact events need not be imagined. They occurred for real between April 1st and May 6th this year. The identity of the bitten coronavirus researcher has not been revealed except that they were working in a high security BSL-3 virus lab when the accident happened. Other researchers are also calling for restraint. In a paper titled "Prudently conduct the engineering and synthesis of the SARS-CoV-2 virus", researchers from China and the US critiqued the synthesis in February of a full length infectious clone (Gao et al., 2020; Thao et al., 2020). And, in concluding, these researchers asked a question that is even more pertinent now than then "Once the risks [of a lab escape] become a reality, who or which organization should take responsibility for them?" The accident at the University of North Carolina (UNC) is now in the public domain but only thanks to a FOIA request submitted by Hammond (in line with NIH guidelines) and shared with Independent Science News. Despite the FOIA request, apart from the fact that UNC classified it as an official "Reportable Incident", i.e. that must be reported to National Institutes of Health (NIH) in Washington DC, scarcely any information about the accident is available. In part this is because the minutes of the relevant IBC meeting (May 6th, 2020, p109) are extremely brief. They do not provide any details of the fate of the bitten researcher. Nor do they state, for example, whether the researcher developed an active infection, nor whether they developed symptoms, nor if they transmitted the recombinant virus to anyone else. Neither do they reveal what kind of recombinant virus was being used or the purpose of the experiment. To try to learn more, Independent Science News emailed the lab of Ralph Baric at UNC, which, based on their research history is the most likely coronavirus research group involved (Roberts et al., 2007; Menachery et al., 2015), the University Biosafety Officer, and UNC Media relations. Only the latter replied: "The April 2020 incident referred to in the University Institutional Biosafety Committee meeting minutes involved a mouse-adapted SARS-CoV-2 strain used in the development of a mouse model system."

"At the dawn of recombinant DNA, at the request of the scientific community itself, following the fabled Asilomar conference, the United States government took the position of not regulating genetic engineering in the lab. The "deal" that big science struck with the government was that, in return for not being directly regulated, principal investigators would take personal responsibility for lab biosafety, involve the public in decision-making, and accept public accountability for their actions. The NIH Guidelines and Institutional Biosafety Committee system of "self-regulation" by researchers is founded upon the principal of personal responsibility of PIs and the promise of transparency. The redaction of the researchers' identities from IBC meeting minutes, in order to hide the activities of researchers and avoid accountability for accidents, fundamentally contradicts the core principles of the US oversight system and violates the commitments that science made. "There is no justification for UNC's redaction of the names of the laboratory heads and the identities of pathogens. UNC's redactions violate conditions UNC agreed to in exchange for NIH funding of UNC's research and, if not corrected, should result in the termination of current NIH funding, and the loss of eligibility for future NIH funding, of UNC's research."

This concern over risks and benefits is shared by Edward Hammond. Using FOIA again he has further discovered that researchers at the University of Pittsburgh (whose identity is redacted) plan to make what Hammond calls Corona-thrax. In short, according to its Institutional Biosafety Committee, Pittsburgh researchers intend to put the spike protein of SARS-CoV-2 (which allows the virus to gain entry into human cells) into *Bacillus anthracis* which is the causative agent of anthrax. The anthrax strain proposed to be used for this experiment is "disarmed" but, Hammond agrees with Gao et al., (2020) that the balance of risks and benefits appears not to be receiving adequate consideration. This experiment was nevertheless approved by the Institutional Biosafety Committee of the University of Pittsburgh. But by redacting the name of the laboratory from the minutes and also every name of the members of the committee which approved it, the University has supplied a de facto response to the final question posed by Gao et al.: who will take responsibility for risky coronavirus research?

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To try to learn more, *Independent Science News* emailed the lab of **Ralph Baric** at UNC, which, based on their research history is the most likely coronavirus research group involved (**Roberts et al., 2007; Menachery et al., 2015**), the University Biosafety Officer, and UNC Media relations. Only the latter replied: "The April 2020 incident referred to in the University Institutional Biosafety Committee meeting minutes involved a mouse-adapted SARS-CoV-2 strain used in the development of a mouse model system." UNC media relations also told *Independent Science News* that: "The researcher did not develop any symptoms and no infection occurred as a result of the incident." Our questions in full and the full UNC reply are [available here](#).

REDACTIONS OF BIOSAFETY COMMITTEE DISCUSSIONS

The second reason for this lack of information is that the UNC redacted the names of Principal Investigators (PIs) whose research required biosafety

scrutiny, along with many of the experimental specifics. Nevertheless, unredacted parts of minutes from IBC meetings held in 2020 contain descriptions of experiments that potentially encompass the accident. They include: Application 75223:

	III-D, BSL-3, plasmids, SARS-CoV-2, mammalian cells, mice	
75223		Generation of a full-length infectious clone of the novel coronavirus (2019-nCoV/SARS-CoV-2) including reporter viruses and mouse-adaptation mutants
	Summary: The objective of this experiment is to generate a reverse genetic system for the newly emerged SARS-CoV-2, (aka 2019-nCoV). The parental wild type (WT) virus was isolated by the CDC and had been passaged three times in Vero cells (GenBank accession #MN179452.1).	

UNC Inst Biosafety Committee Application 75223

(“a full-length infectious clone” refers to a viable DNA copy of the coronavirus, which is ordinarily an RNA virus) and Application 73790:

	III-D, BSL-3, plasmids, mice	
73790		Generation of a full-length infectious clone of a US isolate of the novel coronavirus (2019-nCoV/SARS-CoV-2) including reporter viruses and mouse-adaptation mutants
	Summary: The aim of this experiment is to generate a reverse genetic system for the newly emerged SARS-CoV-2, (aka 2019-nCoV), isolated from a US patient in Washington state. The parental wild type (WT) virus was isolated by the CDC and had been passaged three times in Vero cells (GenBank accession #MN179452.1).	

UNC Inst Biosafety Committee Application 73790

and Application 74962:

	III-D, BSL-3, plasmids, SARS-CoV-2, mammalian and insect cells, mice	
74962		Adaptation of the 2019-nCoV (SARS-CoV-2) infectious clone to mice expressing wild-type mouse ACE2
APPROVED WITH STIPULATIONS	Summary: The purpose of this experiment is to adapt SARS-CoV-2 so that it is able to infect mice carrying wild-type mouse ACE2 (mACE2) through serial in vivo lung passages for development of an animal model to evaluate antivirals and therapeutics and study pathogenicity	

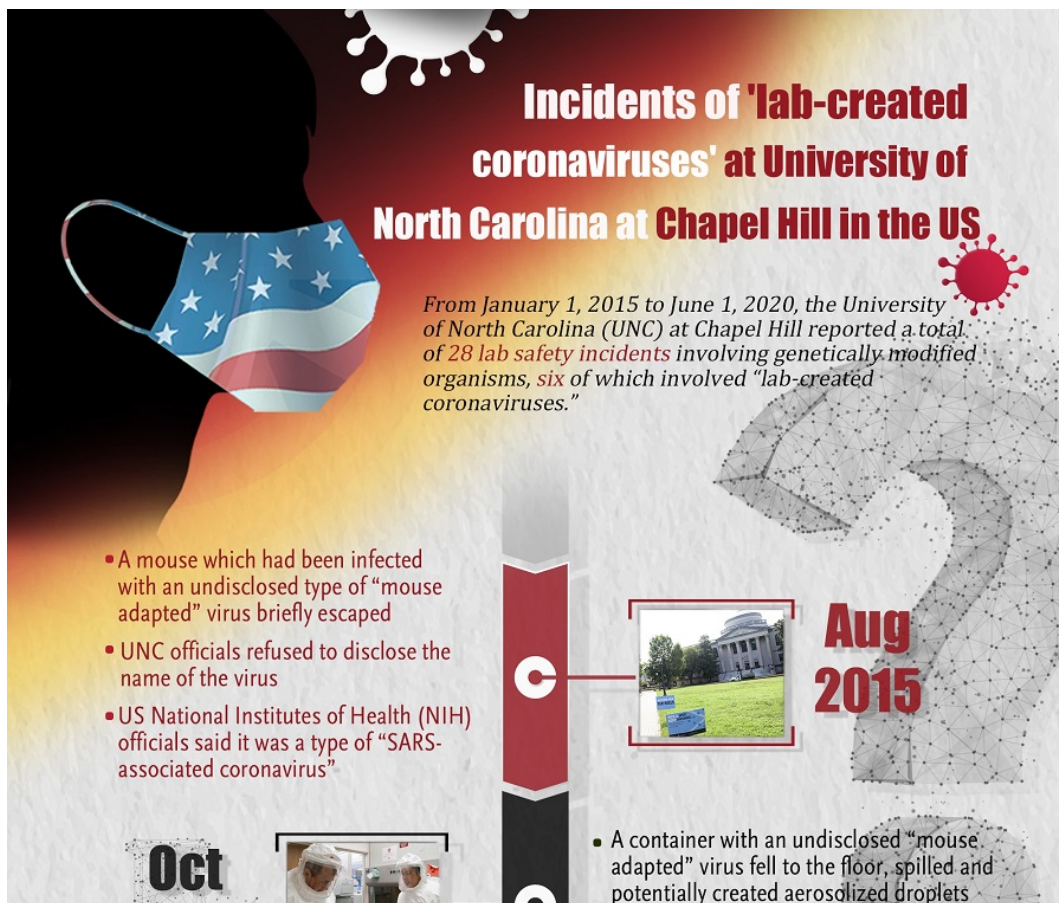
UNC Inst Biosafety Committee Application 74962

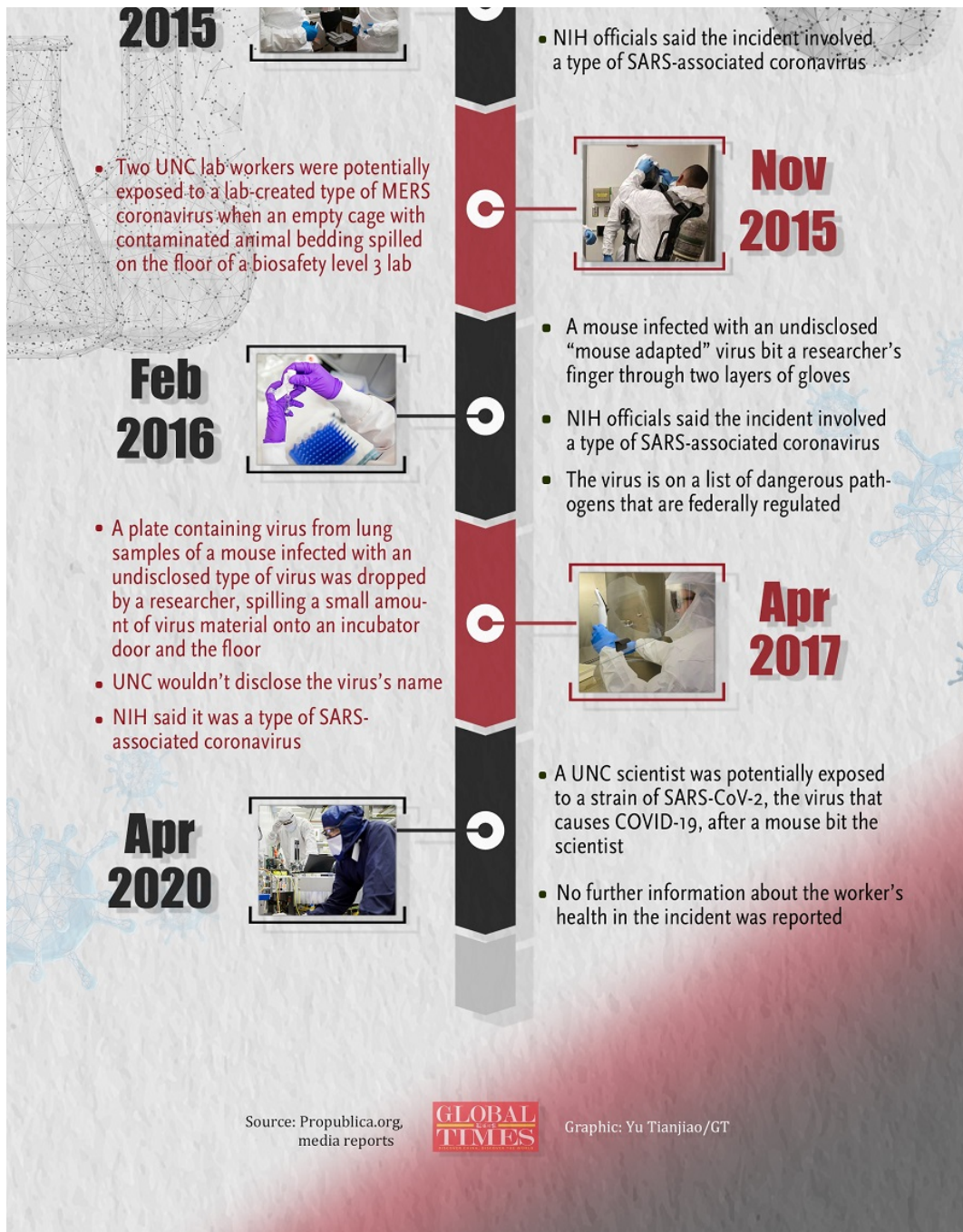
In all, any one of eight sets of different experiments approved by the UNC Chapel Hill IBC in 2020 proposed infecting mice with live infectious and mutant SARS-CoV-2-like coronaviruses under BSL-3 conditions and therefore could have led to the accident.

BARIC SUPPORTS THE ZOO NOTIC THEORY BECAUSE HE PLAYED A PART IN STARTING THE PANDEMIC DUE TO HIS ASSOCIATION WITH WIV SCIENTISTS

MAY 2021 Baric “I really believe that the genetic sequence for sars-CoV-2 really points to a natural-origin event from wildlife,” Ralph Baric said that sars-CoV-2 was different enough from known viruses that to retrofit it from an ancestral strain would have required a truly unprecedented feat of genetic reengineering. And of course you don't know what you're engineering, because SARS-CoV-2 would not have existed.” Another possibility was that a virus nearly identical to the eventual pathogen, which had been collected in the wild and stored in the virus repository, had somehow escaped containment, but he hadn't seen any specific evidence to support that hypothesis, either. All that is known for sure is that a pathogen that likely originated in bats had transferred species and caused a global pandemic in human beings, perhaps in a way that had only happened a few times in modern medical history or in a way—through a lab—that may never have happened before. Baric's preference was for the theory that resembled previous outbreaks.” [Of course Baric would say this since he taught Shi Zhengli how to create viruses in the lab that could not be distinguished from those in nature and so he bears responsibility for the pandemic.]

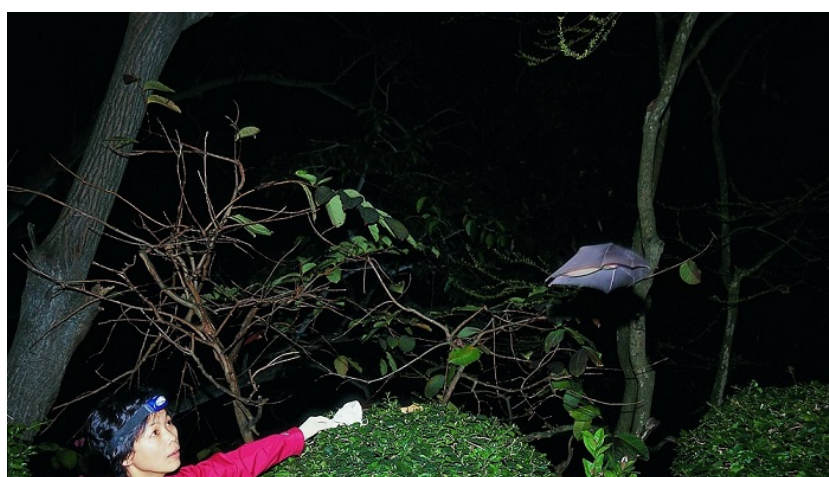
CHICOMS BLAME BARIC





At University of Iowa, scientist Stanley Perlman launched work for the deadly MERS virus without faculty approval, the Des Moines Register reported in December 2014. Worse still, Perlman's team conducted the MERS research in a biosafety level-2 lab, instead of a level-3 facility as is required by federal regulators, it said. [GLOBAL TIMES](#)

THE BAT LADY





SHI ZHENG LI

"THE BAT LADY" NEVER CONDUCTED EXPERIMENTS TO MAKE VIRUSES MORE DEADLY, JUST MORE CONTAGIOUS

Dr. Shi Zheng Li, a WIV Microbiologist and Director of the Centre for Emergence of Infectious Disease and Biosafety at the Wuhan Institute of Virology was known as "The Bat Lady" because of her interest in bats as vectors of disease. Dr. Shi, 57, obtained her Ph.D. from the University of Montpellier in France in 2000 and is a member of the American Academy of Microbiology. Shi was fixated on dirt:

"The pandemic is nature's punishment for an *unsanitary lifestyle*. So shut your *stinky mouths*. How on earth can I offer up evidence for something where there is no evidence? I don't know how the world has come to this, constantly pouring *filth* on an innocent scientist. My lab has never conducted or cooperated in conducting GOF experiments that enhance the virulence of viruses. [Just the transmissability] This is no longer a question of science. It is speculation rooted in utter distrust. It's really sad to read this 'Letter' written by these 18 prominent scientists. The hypothesis of a lab leaking is just based on the expertise of a lab which has long been working on bat coronaviruses which are phylogenetically related to SARS-CoV-2. This kind of claim will definitely damage the reputation and enthusiasm of scientists who are dedicated to work on the novel animal viruses which have potential spillover risk to human populations and eventually weaken the ability of humans to prevent the next pandemic...Another piece of evidence that I can give you is that our lab has been doing research for 15 years, and all our work has been published. We also have a library of our own genetic sequences, and we have experimental records of all our work related to the virus, which are accessible for people to check. Nobody was tested positive. None of us has been infected by coronaviruses under any circumstances, including while sampling bats in the field. I just wanted to put my head down and concentrate on my work, I thought the storm would just blow over after some time. I used to admire the West. I used to think it was a just and meritocratic society. I used to think it must be wonderful to live in a country where anybody could criticize the government. Now I think if you are Chinese then it doesn't matter how good you are at your job—because you are tried by nationality. I've now realized that the Western democracy is hypocritical, and that much of its media is driven by lies, prejudices, and politics."

Dr. Zhengli Shi, Senior Virologist. Dr. Shi will oversee the coronavirus screening for all samples collected in China. Novel SARS-like coronaviruses were detected in *Rhinolophus* bats collected in different regions of Guangdong province. Diverse novel betacoronaviruses related to HKU5 were detected in *Pipistrellus* bats and *laio* in Guangdong and in *Aselliscus stoliczkanus* in Mengla, Yunnan. Novel coronaviruses related to HKU9 were found in *Cynopterus sphinx* and *Rousettus leschenaulti* in Mengla. In addition, sequences significantly divergent to other CoV were obtained from three samples of *laio* and *Hipposideros* bats. "Bats: Depending on the species and size of bat, swabs will be taken from the oropharynx, urogenital tract, and rectum. Fresh feces will be collected if available, in which case a rectal swab will not be collected. Blood will be collected from fruit bats either from the cephalic vein or from the radial artery or vein using a 25 gauge needle and 1 cc syringe. Blood will be collected from bats weighing less than 100g according to published techniques. Principal Investigator/Program Director: Daszak, Peter" [INTERCEPT DOC page 72, 167, 124](#)



SHI ZHENG LI

Daszak's dupe at the WIV was Shi Zheng Li, the director of Bio-Safety. In January 2018, the State Department had visited her lab after reports of unsafe conditions. "During interactions with scientists at the WIV laboratory, they noted the new lab has a serious shortage of appropriately trained technicians and investigators needed to safely operate this high-containment laboratory, [the researchers also showed that various SARS-like coronaviruses can interact with ACE2, the human receptor identified for SARS-coronavirus.](#)" Were the unsafe conditions the fact that the corona virus procedures were being carried out in a low level lab? Doctor Daszak knew the [young Technicians](#) and scientists were incompetent and [sloppy](#). He knew Shi Zheng Li, "The Bat Lady" was a weirdo. Interestingly enough Shi stated that no experiments were conducted at the WIV to make the virus more deadly but never addressed the experiments that made it more contagious. Daszak put her in touch with the genius Dr. Ralph Baric and, with him, she co-authored a paper on SARS-1 coming from bats. Baric developed a method to alter the RNA in a virus by cutting the strands in separate sections then re-combining them with other viral RNA. This man is more dangerous than Daszak because he has the ability to make a virus more lethal, but his motivation is to create vaccines, not a pandemic. In summation, Daszak who was at the epi-center of all this activity, knew how risky to humanity these WIV activities were and made sure they were conducted.

TRUMP AND BIDEN BOTH SAY GET VACCINATED AGAINST THE DASZAK STRAIN



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REPORTER: "800,000 coronavirus deaths — do you have a statement on your responsibility? And why haven't you asked China to do more, to be transparent on the origins?"

BIDEN: *smiles, walks away*



TWO WUHAN INSTITUTE OF VIROLOGY SCIENTISTS, XING-YI GE AND ZHENGLI-LI SHI, USE REVERSE GENETICS TO GENERATE A CHIMERICAL VIRUS CLOSELY RESEMBLING THE NOVEL CORONAVIRUS COVID-19 (WHY COULDN'T THEY HAVE DEVELOPED THE NOVEL CORONA VIRUS?)

MAY 13, 2020: Two Wuhan Institute of Virology scientists, Xing-Yi Ge and Zhengli-Li Shi, use reverse genetics to generate a chimeric virus (one that has been created by combining cells of more than one distinct genotype) closely resembling the novel coronavirus Covid-19: "On the basis of these findings, we synthetically re-derived an infectious full-length SHC014 recombinant virus and demonstrate robust viral replication both in vitro and in vivo." The Nature Medicine article also mentions, "Human lungs for HAE cultures were procured under University of North Carolina at Chapel Hill Institutional Review Board-approved protocols." The Chinese government's poor record of transparency; the fact that the Wuhan Institute of Virology, a research center with facilities in the same city where the virus first appeared, was studying and creating new dangerous pathogens, including bat coronaviruses cannot be easily dismissed.

If the virus leaked out of a Chinese lab, every one through four Bio-Safety Level laboratory in the U.S. and Europe will be shut down and forced to move to more isolated locations. In 2010, by one count, there were 249 BSL-3 laboratories and seven BSL-4 laboratories in the U.S., and more than 11,000 scientists and staffers were authorized to handle the ultra-lethal germs on the government's select pathogen list. Jamie Metzl of the Asia Society: "If zoonosis was the origin, it was a validation of Dr. Daszak's life work. But if the pandemic started as part of a lab leak, it had the potential to do to virology what Three Mile Island and Chernobyl did to nuclear science. It could mire the field indefinitely in moratoriums and funding restrictions." So many virologists are [circling the wagons around Fauci](#) because of this and because he is the one the issues them their research grants.



YOUNG BAT LADY

In January 2021 the CCP called her "a non-party person" which is highly unlikely, considering the status of the position she reached. The CCP did this in order to distance it from her in case the truth surfaces.

<http://www.hbkk.org.cn/ztzl/2020/zmkjgzz/info?newsid=579719f583574e0ca72e0e590366efbd>

ANOTHER KEY FIGURE TO EMERGE IN THIS DEBACLE IS ALEKSEI CHMURA





Chmura was educated at Kingston University Academic degree Doctor of Philosophy start time September 1, 2012 end time June 1, 2018; Columbia University academic degree Bachelor of Science Start time September 1, 2001 end time May 15, 2004. I call him Chumpura.

This is from a book that mentions Chumpura: "Quammen then narrates the race to identify the SARS agent and its (still) elusive reservoir host. Finally he joins Aleksei Chmura, an American virus hunter-cum-global gourmand. As a prelude to their fieldwork, the two men bond over clotted pig's blood, bean sprouts, red peppers, and drippy globs of durian, "the world's stinkiest fruit." Then it's off—minus protective respiratory gear—to netting bats in the karst mountains near Guilin and later phlebotomizing them. Wrapping the chapter is an excursion to a cinderblock billet in southern China where Farmer Wei Shangzheng raises placid bamboo rats headed for human dinner plates". [Am. J. Trop. Med. Hyg., 88(4), 2013, pp. 803–805 doi:10.4269/ajtmh.13-0092 Copyright © 2013 by The American Society of Tropical Medicine and Hygiene Serological Evidence of Bat SARS-Related Coronavirus Infection in Humans, China. Wang N1, Li SY2, Yang XL1, Huang HM2, Zhang YJ1, Guo H1, Luo CM1, Miller M3, Zhu G3, **Chmura AA3**, Hagan E3, Zhou JH4, Zhang YZ4, Wang LF5, **Daszak P3**, Shi ZL1]

<https://europepmc.org/article/PMC/6178078>

ALEKSEI CHMURA & PETER DASZAK'S ECO-FASCIST MANIFESTO

They seem to go back quite a long way Daszak helped supervise his Thesis. They wrote a quite bizarre letter back in 2007 called "[A FALL FROM GRACE TO...VIRULENCE?](#)"



"A FALL FROM GRACE TO...VIRULENCE?" PETER DASZAK CORRESPONDING AUTHOR AND ALEKSEI CHMURA

In Bruegel's painting of The Fall of the Rebel Angels we are witness to a tumbling maelstrom of falling rebel angels outcast from Heaven. Within the fray stands St. Michael¹ in gilded armor, and his angels-at-arms serenely in pale albs, and almost as if threshing grain, hewing and striking down this inconceivable rout. The main focus of the image and what draws the eye is the extraordinarily creative mélange of creatures; mixtures of human, animal, plant, and inanimate objects slashing and stabbing as they fall from the great battlefields in the skies. They pour down in a vast column that stretches infinitely from the luminous sun; they fall from the light to the darkness. The column of falling angels is so numerous that it widens to encompass the whole lower canvas as it approaches the viewer. With a start, then, we realize that Bruegel intends that we too are in the thick of this. **Will we succumb to the multitudinous horde? Are we to be cast downward into chthonic² chaos represented here by the heaped up gibbering phantasmagory³ against which we rail and struggle?**

1. Saint Michael is an archangel, a spiritual warrior in the battle of good versus evil. He is considered a champion of justice, a healer of the sick, and the guardian of the Church. In art Saint Michael is depicted with a sword, a banner, or scales, and is often shown vanquishing Satan in the form of a dragon.

2. Concerning, belonging to, or inhabiting the underworld.

3. A fantastic sequence of haphazardly associative imagery, as seen in dreams or fever.

Clearly Bruegel intended for us to identify with St. Michael and his comrades. The classic imagery of religious battles between humanity and evil, is straightforward fodder for us to digest, but is there another metaphor here? **If the fallen angels [depicted in the Bruegel painting] represent the evil mirror image of St. Michael and his cohort, so they also represent the mirror image of our own genetic kind—pathogenic organisms which are otherwise just like us, but have fallen from grace through an evolutionary (not spiritual) pathway that takes them to a netherworld where they can feed only on our genes, our cells, our flesh.** On closer scrutiny, we can see that Bruegel has depicted the Natural World—specifically chosen it as proxy for the fallen angels—for both its fascinating wonder and horror. Thus may we surmise that nature was, in Bruegel's mind, itself as strange, wondrous, and horrific as the fallen angels that he depicted in the juxtaposed forms of otherwise anatomically correct fishes, bats, and frogs? Bruegel was an urban man and precisely because of his lack of intimate knowledge of Nature, he was likely able to observe it with such precision. No doubt he was influenced during time spent in France & Italy by that unique Renaissance creation, the scientific method, or means to learn about phenomena via empirical evidence. Today, we are not unlike Bruegel as we view the wondrously diverse animals and plants that represent nature, peering beneath this palimpsest the pathogens that threaten to plague us? AIDS, SARS, Malaria, West Nile Virus, and Avian Influenza are but a few of these fallen angels that have burst from out of the Natural world to wreck havoc causing countless deaths and economic losses.

In Bruegel's curious chimeras, we find yet another analogy—for the genetic recombination, mutation and evolution that negative-stranded RNA viruses in particular undergo as they shift, morph and adapt to their changing habitat—animal cells. Here St. Michael is at risk of more than just the prodding of a sword. Here he is at the mercy of the tooth and nail of glycoproteins sharpened and honed to strike with precision

through the gaps in his golden armor. As Pulliam shows in this issue of EcoHealth, this battle continues in reality as human encroachment into wildlife habitat, and the increasing globalization of agriculture, trade and travel bring us into dramatic juxtaposition with a seemingly infinite number and variety of viral angels hosted by the wildlife we contact and exploit. In this prescient scene, Bruegel reminds us that our battle against novel zoonotic pathogens is far from over: They lie in wait in a multitude of surely the same overwhelming dimensions as Bruegel's column of descending angels. Perhaps he reminds us also that it is the nature of our interactions with wildlife—here represented as an evil entity for humanity to vanquish—which cause new zoonoses to emerge in the first place. Perhaps the EcoHealth view is that if we tread carefully, we might avoid those nasty little pincers waiting to nip!

[Another manifesto - this one decrying the Industrial Revolution](#)

CHAPTER 6

NAZI SCUM BOHDAN DASZAK MAKES THE ECO-FASCIST CHARGE CREDIBLE



PETER DASZAK

DASZAK grew up with a hard core Nazi, his father, Bohdan Daszak, a rabid Jew hating scum and former member the OUN Youth, (Organization of Ukrainian Nazis or "Nationalists"). Peter Daszak is the son-of a Nazi death camp executioner who volunteered to murder countless Jews, and like father like son. Daszak was indoctrinated in Nazi thought by this Nazi war criminal: While protecting flora, fauna, water, and soil, the Nazis also murdered millions of human beings. The Christchurch mass murderer manifesto: ["I consider myself an Eco-fascist by nature. The nation with the closest political and social values to my own is the People's Republic of China."](#) As documented here, [Daszack is an agent-of-influence for the Chinese Communist Party](#), who led the W.H.O. cover-up. Daszak never says not a bad thing about China, including commenting on their human rights abuses, such as building concentration camps for the Uyghurs. Daszak was taught to respect fascism: like that of the CCP and his father had taught him concentration camps were okay. **Daddy and China** are keys to the fact that he is something other than what he pretends to be. [Read what Facebook members comment about him!](#)

DASZAK'S FATHER, BOHDAN DASZAK, WAS A NAZI DEATH CAMP EXECUTIONER



REICHSFUEHRER SS HEINRICH HIMMLER TOURING [JANOWSKA DEATH CAMP](#) LEMBERG, DISTRICT OF GALICIA, GENERAL GOVERNMENT (FORMERLY LWÓW, SECOND POLISH REPUBLIC; TODAY LVIV, UKRAINE). OPERATED BY SS OPERATIONAL SEPTEMBER 1941 – NOVEMBER 1943 INMATES JEWS

In September 1941, the Germans set up a factory on Janowska Street in the northeastern suburbs of Lvov, in southeastern Poland. This factory became part of a network of factories, the German Armament Works, owned and operated by the SS. Jews were used as forced laborers, mainly in carpentry and metalwork. In October 1941, the Germans established a camp housing the forced laborers next to the factory. In addition to being a forced-labor camp for Jews, Janowska was a transit camp during the mass deportations of Polish Jews to the killing centers in 1942. Jews underwent a selection process in Janowska similar to that used at Auschwitz-Birkenau and Majdanek. Those classified as fit to work remained at Janowska for forced labor. The majority, rejected as unfit for work, were deported to Belzec and killed or were shot at the Piaski ravine, just north of the camp. In the summer and fall of 1942, thousands of Jews (mainly from the Lvov ghetto) were deported to Janowska and killed. The evacuation of the Janowska camp began in November 1943. As the Germans attempted to destroy the traces of mass murder (Aktion 1005), they forced the prisoners to open the mass graves and burn the bodies. On November 19, 1943, these prisoners staged an uprising and a mass escape attempt. A few succeeded in escaping, but most were recaptured and killed. **The SS staff**

and their local auxiliaries murdered at least 6,000 surviving Jews from various forced-labor camps in Galicia when the Janowska camp was liquidated in November 1943. <https://ukrainianjewishencounter.org/en/the-janowska-concentration-camp-what-we-know-and-dont-know/>



The day began with an inspection that culminated in mass beatings and shootings of prisoners. The weak, the sick, and those who had violated discipline were either shot on the spot or brought to the area between the two barbed wire fences, where they were shot or simply expired. Death runs were also carried out. This meant that a large group of condemned prisoners had to run the gauntlet of SS men, who tripped them with their legs or carbines, beat them over the head, shot at them, etc. There were two gallows in the camp. One of them was for prisoners who wanted to commit suicide. Every day the prisoners were subjected to abuse and beatings for no reason. There is evidence indicating that every day nearly a hundred corpses were piled on the garbage dump next to the kitchen. In other words, this was a daily, systematic killing of people, but the methods used were quite different. Special methods were used to kill women, and we have testimony about sexual violence and crimes in the camp.



Peter Daszak's brother, opera singer John Daszak, revealed: "My father, Bohdan Daszak, (born March 21, 1926 died February 5, 1996 in Tameside, Greater Manchester, England) was a Ukrainian who had ended up in Britain at the end of the Second World War. **Thankfully for him he was taken prisoner by the Allies and later released into the community rather than sent back to Ukraine and be dispatched with.** He ended up in Manchester where I was born after he married a British woman, she was half Welsh and half English – so technically I am only a quarter English [laughs]. So I was brought up here but never really felt I always fitted in. It was only when I started travelling around I realised why my father was so culturally very different to those around me."

<https://seenandheard-international.com/2013/09/newjohn-daszak-genesis-of-a-new-british-siegfried-an-interview-with-jim-pritchard>

FROM GIFTED LIVES BY JOAN FREEMAN

John Daszak not only had a powerful mother, but his father, Bogdan Daszak, had lived a life of exceptional bravery and determination. He had managed the extraordinary feat of reaching England from the Ukraine during WWII.[As a Prisoner-of-War] When he was about 16, in March 1944, the German's had occupied his country. They captured him by going round the villages threatening to shoot the families unless the sons joined the German army. At that time the boys hated the Russians even more, and so were willing to join the the German's who were fighting the Russians. But since the Russians and become allies of the British, the boys became enemies of the British. Many who had been badly treated ran off and escaped. **Bogden though was an educated town boy, not a peasant like the others, so he was used for paperwork in a [Nazi death] camp.**¹ He was eventually taken as a POW by the British. He could not know whether his family was alive, nor could he try to contact them because he knew that if someone found out his was alive, they would torture his family. In fact Bogdan's father was tortured by the Russians. About 40 years later, in the mid-1980's, a friend spotted the name Zenon Daszak in a magazine and told Bogdan, who was thrilled to find his long lost brother alive. Zenon he said, was always practicing the violin, and though he'd preferred football himself, and he used to laugh at his brothers devotion. Zenon had become head of music Conservatories in Lvov in the Ukraine, their home town, and had played in the Bolshoi orchestra. Lvov was at the time under Soviet rule and it was forbidden for a Westerner to openly contact someone there. Bogdan though managed to pass his brother a secret message, along with his childhood pet name that no one else would know. They met in 1989 in Munich where Zenon was adjudicating at an international string competition. This had to be in secret shaking off the KGB. Zenon had named one of his sons Bogdan. Another one of his sons Uri had become a well known viola player. Both brothers died in their 60's and John no longer and John no longer has contact with Zenon's family. It had been particularly important to Bogdan that his family became totally British. He forbade them from visiting the Ukraine.

https://www.google.com/books/edition/Gifted_Lives/ySIiCK3A4uEC

Public prosecutors in Germany have indicted a 95-year-old woman for her role supporting the Nazi killing machinery as a secretary in a concentration camp, charging her with 10,000 counts of being an accessory to murder, and complicity in attempted murders. The indictment against the woman, identified only as Irmgard Furchner under German privacy laws, followed a five-year investigation, prosecutors said. Because she was under 21 at the time of the offenses she is accused of, they said, she would be tried in a juvenile court, where she is likely to receive a milder sentence. The woman worked between June of 1943 and April of 1945 as a secretary for the camp commander at the Stutthof camp, 20 miles from the Polish city of Gdansk, which was known as Danzig under German rule at the time. "It's about the concrete responsibility she had in the daily functioning of the camp," said Peter Müller-Rakow of the public prosecutor's offices in Itzehoe, north of Hamburg. [NYT](#)

Those Ukrainians who did collaborate with the German occupiers did so in various ways including participating in the local administration, in German-supervised auxiliary police, Schutzmannschaft, in the German military, **and serving as concentration camp guards.** Nationalists in western Ukraine were among the most enthusiastic and hoped that their efforts would enable them to re-establish an independent state later on. For example, on the eve of Operation' Barbarossa, as many as 4000 Ukrainians, operating under Wehrmacht orders, sought to cause disruption behind Soviet lines. After the capture of Lviv, a highly-contentious and strategically-important city with a significant Ukrainian minority, OUN [Organization of Ukrainian Nationalists], leaders proclaimed a new Ukrainian State on June 30, 1941 and simultaneously encouraged loyalty to the new regime in the hope that they would be supported by the Germans. Already in 1939, during the German-Polish War, the OUN had been "a faithful German auxiliary." Few people noticed when they arrived in Britain in May 1947: one Labour MP, Barnett Janner, complained bitterly in the Commons that members of the Galizien division "murdered hundreds of people in cold blood", while a solitary letter in the *London Evening News*, signed with the correspondent's death camp number,

3399, complained that he or she had witnessed first-hand the "brutal, uncouth and bloodthirsty" behaviour of Ukrainian guards. Most newspapers devoted just one paragraph to reporting the division's arrival, however. The men were dispersed among PoW camps. Over the next three years just eight "undesirables" were deported to Germany, while some emigrated to Canada, the US or Argentina.

Daszak knew the viruses had leaking potential leading to a pandemic yet he did nothing even after the State Department deemed the WIV unsafe he continued funding the bat virus and collection work. A pandemic would delay human encroachment on nature. Daszak favors plant and animal life over human life. Daszak is not only an eco-fascist, but a eco-Fascist mole or eco-Fascist spook. What this means is that you can't tell where he is coming from, from his social media. He is not connected to the rightwing and has embedded himself in the Democratic Party.

DASZAK'S FATHER, BOHDAN, WOULD BE PROUD OF HIM



SCIENCE MAGAZINE VERSION

Daszak grew up in Dukinfield, England, a coal-mining town outside of Manchester. **His father was a Ukrainian conscripted to serve in the German army when the Nazis invaded who wound up a British prisoner of war in Italy, which eventually led him to Scotland and a job in a chocolate biscuit factory.** He later worked as a draftsman and married a woman from Dukinfield. Daszak had 18 cages of reptiles at home. "I'm a lizard guy," he says. In a primary school essay, he wrote that he wanted to become a zoologist and study marmosets in the Amazon. He studied zoology at Bangor University and earned a Ph.D. in infectious diseases at the University of East London with a thesis on electron microscopy of a parasite that caused an intestinal disease in chickens. **A postdoctoral** [Daszak worked at the School of Life Sciences, Kingston University, in Surrey, England in the 1990s. He never earned a post-graduate degree [Wiki](#)] stint at Kingston University led to a collaboration with former surgeon Andrew Wakefield, now infamous for his role in the antivaccine movement."

LIKE DEMJANJUK DID BOHDAN DASZAK SERVE AS AN EXECUTIONER AT SOBIBOR EXTERMINATION CAMP IN POLAND?

Naturalisation Certificate: Bohdan Daszak. From Poland. Resident in Dukinfield,...

Ordering and viewing options

Reference: HO 334/436/60527

Description:

Naturalisation Certificate: Bohdan Daszak. From Poland. Resident in Dukinfield, Cheshire.

Certificate BNA60527 issued 26 April 1960.

Date: 1960 Apr 26

Held by: The National Archives, Kew

Legal status: Public Record(s)

Language: English

Closure status: Open Document, Open Description

	Größe: 175 cm	Empfangene Ausrüstungsgegenstände	
	Gesichtsform: oval	Mütze: 1	Koppel: 1
Haarfarbe: dunkelblond	Mantel: 1	Seitengewehr-tasche: 1	
Augenfarbe: grau	Bluse: 1	Handschuhe: 1	
Besondere Merkmale: Narbe auf dem Rücken	Hose: 1	Unterhemd: 1	
	Stiefel: 1	Unterhosen: 1	
	Schnürschuhe: 1	Wollweste: 1	
	Socken: 1	Badehose: 1	
	Fusslappen: 1		
	Essgeschirr: 1		
	Brotbeutel: 1		
	Trinkbecher: 1		
	Feldflasche: 1		
	Wolldecken: 1		
	Gewehr Nr. 1		

Born in 1920 in Soviet Ukraine, John Demjanjuk was conscripted into the **Soviet Red Army** in 1940. He fought in World War II and was taken prisoner by the Germans in spring 1942. He was recruited by the Germans and trained at **Trawniki concentration camp**, going on to serve at Sobibor extermination camp and at least two concentration camps. After the war he married a woman he met in a West German displaced persons camp, and emigrated with her and their daughter to the United States. They settled in Seven Hills, Ohio where he worked in an auto factory and raised three children. Demjanjuk became a US citizen in 1958.

CHAPTER 7

DASZAK COLLABORATED WITH A NOTORIOUS ANTI-VAXXER



Wakefield asked Daszak to do electron microscopy of gut segments removed from Crohn disease patients. They found evidence of the measles virus, and Wakefield—"a charismatic guy," Daszak says—went on to argue that the measles vaccine might be to blame for the disease. Subsequent studies made Daszak question the findings. "No one could repeat it," he says. Wakefield was later discredited for a fraudulent study that linked vaccines to autism and has become a touchstone for vaccination skeptics. Daszak had 18 cages of reptiles at home. "I'm a lizard guy," he says. In a primary school essay, he wrote that he wanted to become a zoologist and study marmosets in the Amazon. He studied zoology at Bangor University and earned a Ph.D. in infectious diseases at the University of East London with a thesis on electron microscopy of a parasite that caused an intestinal disease in chickens. [Science](#)

CHAPTER 8

DR. DASZAK'S HIDDEN AGENDA

Daszak financed DURC [Dual Use Research of Concern \(DURC\)](#) procedures. The DURC experiments involved creating new forms of life, just as Mary Shelly's Doctor Frankenstein did when he created a homicidal monster. But the chance of creating a monster virus didn't bother "Dr. Daszakstein," who headed a "non-profit" called [EcoHealth Alliance](#), because it was Doctor Daszak's intention from the start to cause a pandemic. [Dr. Daszak is not a microbiologist](#). Daszak has no medical degree. None-the-less he plays a major part in the most dangerous experiments known to man. He's a world-class conman with a British accent and a hidden agenda, as stated, the son of a [Nazi war criminal, a Ukranian who volunteered to kill Jews in a notorious death camp](#). Daszak never talks about the father who raised him, Bohdan. As for December 2021 Peter Daszak murdered 5 million including many Jews - and counting.....Experts say that five million is an undercount. Many countries are unable to accurately record the number of people who have died from Covid-19, like India and African nations. It took nine months for the virus to kill one million people, three and a half more to reach two million, another three to claim three million and about two and a half to exceed four million. Feb. 4, 2022 More than 2,600 Americans are dying from Covid-19 each day, an alarming rate that has climbed by 30 percent in the past two weeks. Across the United States, the coronavirus pandemic has now claimed more than 900,000 lives.

DASZAK FOCUSED ON GAIN-OF-THREAT, GAIN-OF-FUNCTION RESEARCH FOR A REASON

DASZAK: "If we do the math on the previous emerging disease events the viruses tend to come from animals. Mammals cover the vast majority. You should probably include birds, because of Avian flu being such a threat. It is a stamp collecting exercise. Some of those stamps are penny blanks and you have to throw them out. Some of the viruses will be killers and some of them won't. How do we work that out from a viral sequence? It is not straight forward. First of all we are only looking at viral families that include those that have gotten to people from animals. We have narrowed it down from there. Then, when you get a sequence and it looks like a relative to their known nasty pathogen just like we did with SARS – we found viruses in bats. Some of them looked very similar to SARS. **We sequenced the spine protein, the protein that attaches to cells, and then you create pseudo particles, insert proteins from the viruses that combined to human cells. Each step of this you move closer and closer to could the virus becomes pathogenic in people! You narrow down the field. You end up with a small number of viruses that really do look like killers.** And you look at the people in the region where the animal lives; do we see anti-bodies to that virus? In Cameroon it was a new virus coming into people. What is the activity and can we find the alternative? It is not straight forward, but there are many ways to hone it down. We had just got to do it. *It makes sense for humanities sake.*" [See video](#)

Daszak : "We found corona virus in bats which looked exactly like SARS....My colleagues in China [at the Wuhan Institute of Virology] did this work, you create pseudoparticles¹, you insert the spike proteins from those viruses, see if they bind to human cells and each step of this you move closer and closer to: [a virus could really become pathogenic in people.](#)" Most of the experiments with bat viruses were performed with wild-type viruses.

1. Pseudotypes are biosafe, replication-defective retroviruses and lentiviruses that have been repurposed from gene therapy applications. They have heterologous (foreign) viral glycoproteins on their surface that originate from the viral pathogen. They thus mimic the wild- type virus with respect to cell entry, but can be handled by end users in biosafety level (BSL)-1 instead of BSL-3/4 laboratories. "Experience working with receptor mutants & pseudovirus binding assays: We have established a stable pseudovirus assay for SARS-CoV and SARS-like CoV and tested the infectivity of these spike proteins in cells expressing ACE2 from human, civet and bats (52, 68). We have demonstrated that several bat species are susceptible to the SARS-CoV and that some SARS-like CoV strains can use human ACE2 for cellular entry (Intercept 125) Minor mutations in S proteins or ACE2s greatly affected the receptor binding and finally abolish the pseudovirus entry (68, 121) (Fig. 9). Recently, we have discovered a number of alpha and beta CoVs including HKU4/5

We will use prepared pseudoviruses bearing different S proteins to infect human and bat ACE2 or DPP4 receptor expressing cells (in Hela cell model), 24 hours post infection, receptor usage by different S proteins will be determined by measuring luciferase activities. We will also induce site mutations in S proteins using site-directed mutation method, then do receptor-mutant pseudovirus binding assays. Pseudovirus infectivity on different human cell lines (A549, 293T, Caco, Huh?. and etc), primary and immortalized bat cell lines (listed below) and other mammalian cell line (mouse, pig, hamster, monkey, and ect) will be also determined by luciferase assay. The results will provide information

whether bat-CoVs could use known bat and human ACE2. DPP4 or other known CoV receptors to enter cells. and allow us to determine critical receptor binding sites. viral host range, and to better predict the capacity of our Co Vs to infect people. (Intercept 118)



Daszak continued to finance the collection of exotic bat viruses and GoF / GoT experiments that were being performed in a low level biosecurity lab at the WIV - despite the fact they were banned in the USA and despite the fact he was not a microbiologist. Daszak knew if GoF / GoT procedures were banned in the USA, where bio-security was high, they should not be out-sourced to China, where he knew first hand bio-security was minimal. Any normal person in Daszak's position would have seen red flags. But Daszak had a hidden agenda which was to start a pandemic, so he ignored them. The U.S. House of Representatives Foreign Affairs Committee: **"Was Daszak aware the funding he was providing directly supported gain-of-function research by paying for the collection of viruses the Wuhan Institute of Virology (WIV) later experimented with, even though the federal government had a moratorium on GoF research from 2014 through 2017?"** Either a bat virus escaped that could directly infect humans or these procedures created a novel bat virus whose spike protein was genetically engineered to easily interface with the human respiratory system's ACE2 receptors, ostensibly to determine in which species of bat the next spillover to humans would occur. Daszak had predicted that a new virus would arise from a spillover. He called it VIRUS X. The enhanced natural bat virus that Daszak's crew created, or natural one they collected, escaped the Bio Safety Lab-2 facility, that had a much security as a dental office, and caused a pandemic setting back civilization God knows how long? Or the virus was one of the known bat-CoVs (including 630 novel CoV sequences) collected and stored at the WIV. Daszak puts the collection figures much higher. Perhaps it was the **Rhinolophus Horseshoe virus or RaTG13 or RmYN02 that was altered?** The virus was bio-engineered to be more contagious, not more virulent, accounting for the number of mild cases, before it began to mutate into something more deadly, such as **"the Delta Mutation."** The Delta Variant causes mucormycosis, Black Fungus, a rare and often deadly disease that has exploded across India on the coattails of the coronavirus pandemic. 44% of new Covid cases in NYC are attributable to this mutation. Fully immunized people with breakthrough infections of the Delta variant can spread the virus to others just as readily as unvaccinated people. The Alpha variant proved to be twice as transmissible as the original virus, and the Delta variant has mutations that turbocharged its contagiousness even more. As the virus continues to change, newer variants may turn out to be even more transmissible. In early August 2021 in Wuhan, the authorities started testing all 12 million residents after only three cases of the Delta variant were discovered. The cities of Sanmenxia and Zhuhai have also begun mass testing. In Beijing, where there are five infections, train service from 23 cities has been canceled. In the U.S. "This Delta wave just rips through the unvaccinated," said Howard Markel, a medical historian at the University of Michigan. The deaths that have followed the wide availability of vaccines, he added, are "absolutely needless." The variant is thought to be more contagious than previous versions of the coronavirus because the infected carry it in substantially greater amounts in their airways.

HIDDEN AGENDA: CUT DOWN ON HUMAN POPULATION GROWTH THAT'S DESTROYING NATURE

Over all, the birthrate declined by 4 percent in 2020. Births were down most sharply in December 2000, when babies conceived at the start of the pandemic would have been born. The New York Times reported: "All over the globe, countries are confronting population stagnation and a fertility bust, a dizzying reversal unmatched in recorded history. Fewer babies' cries. More abandoned homes. **Toward the middle of this century, as deaths start to exceed births, changes will come that are hard to fathom.**" When one of SHI, BARIC, DASZAK designer viruses escaped, 3,840,528 people died and 177,559,790 were infected. In the United States, life expectancy fell by a full year in the first six months of 2020; for Black Americans, the drop was 2.7 years. [Daszak employs no blacks at his Eco-Health Alliance operation.] December 2020 had the single largest decline of any month. Over all for the year, births declined by 4 percent, the data showed. There were 3,605,201 births in the United States last year, the lowest number since 1979. The International Monetary Fund predicts that the global economy will lose over \$22 trillion between 2020 and 2025. A major part of Eco-Fascism's agenda was fulfilled. To an ecofascist, in order to achieve both environmental and social purity, people of color and immigrants must sacrifice themselves for the good of the planet. From 2019 to 2020, Hispanic people experienced the greatest drop in life expectancy — three years — and Black Americans saw a decrease of 2.9 years. White people experienced the smallest decline, of 1.2 years. Deaths exceed births in Alabama Nearly 15 million more people died during the pandemic than would have in normal times, the World Health Organization said a staggering measure of Covid's true toll that laid bare how vastly country after country has undercounted victims. April 26, 2022: Sixty percent of Americans, including 75 percent of children, had been infected with the coronavirus by February 2022, federal health officials reported — another remarkable milestone in a pandemic that continues to confound expectations. The highly contagious Omicron variant was responsible for much of the toll. Global cases surpass 400 million! The number of women in the United States who died during pregnancy or shortly after giving birth increased sharply during the first year of the coronavirus pandemic, according to a new study, an increase that health officials attribute partly to Covid and pandemic-related disruptions. The new report, from the National Center for Health Statistics, found that the number of maternal deaths rose 14 percent, to 861 in 2020 from 754 in 2019. Black women in America experienced the most deaths: One-third of the pregnant women and new mothers who died in 2020 were Black, though Black Americans make up just over 13 percent of the population. Their mortality rate was nearly three times that of white women. By May 15, 2022 one million Americans had died, including my first wife, Ann Christine Duncan-Weberman. CDC reported: <https://www.cdc.gov/nchs/data/hestat/maternal-mortality/2020/maternal-mortality-rates-2020.htm>

DASZAK FINANCED WIV GAIN-OF-THREAT EXPERIMENTS WITH YOUR TAXPAYER MONEY

Form 990 (2016)		Page 10	
Part IX Statement of Functional Expenses			
Section 501(c)(3) and 501(c)(4) organizations must complete all columns. All other organizations must complete column (A).			
Check if Schedule O contains a response or note to any line in this Part IX <input type="checkbox"/>			
Do not include amounts reported on lines 6b, 7b, 8b, 9b, and 10b of Part VIII.	(A) Total expenses	(B) Program service expenses	(C) Management and general expenses
1 Grants and other assistance to domestic organizations and domestic governments. See Part IV, line 21.	1,199,654	1,199,654	
2 Grants and other assistance to domestic individuals. See Part IV, line 22.			
3 Grants and other assistance to foreign organizations, foreign governments, and foreign individuals. See Part IV, line 15 and 16.	3,622,691	3,622,691	

Form 990 (2017)		Page 10	
Part IX Statement of Functional Expenses			
Section 501(c)(3) and 501(c)(4) organizations must complete all columns. All other organizations must complete column (A).			
Check if Schedule O contains a response or note to any line in this Part IX <input type="checkbox"/>			
Do not include amounts reported on lines 6b, 7b, 8b, 9b, and 10b of Part VIII.	(A) Total expenses	(B) Program service expenses	(C) Management and general expenses
1 Grants and other assistance to domestic organizations and domestic governments. See Part IV, line 21.	2,586,198	2,586,198	

2 Grants and other assistance to domestic individuals See Part IV, line 22	0			
3 Grants and other assistance to foreign organizations, foreign governments, and foreign individuals See Part IV, line 15 and 16	4,232,789	4,232,789		

Form 990 (2018)

Page **10****Part IX Statement of Functional Expenses**

Section 501(c)(3) and 501(c)(4) organizations must complete all columns. All other organizations must complete column (A).

Check if Schedule O contains a response or note to any line in this Part IX ☐

Do not include amounts reported on lines 6b, 7b, 8b, 9b, and 10b of Part VIII.	(A) Total expenses	(B) Program service expenses	(C) Management and general expenses	(D) Fundraising expenses
1 Grants and other assistance to domestic organizations and domestic governments See Part IV, line 21	1,388,318	1,388,318		
2 Grants and other assistance to domestic individuals See Part IV, line 22	0			
3 Grants and other assistance to foreign organizations, foreign governments, and foreign individuals See Part IV, line 15 and 16	5,428,158	5,428,158		

Did the organization have aggregate revenues or expenses of more than \$10,000 from grantmaking, fundraising, business, investment, and program service activities outside the United States, or aggregate foreign investments valued at \$100,000 or more? If "Yes," complete Schedule F, Parts I and IV. YES

Did the organization report on Part IX, column (A), line 3, more than \$5,000 of aggregate grants or other assistance to or for foreign individuals? If "Yes," complete Schedule F, Parts III and IV. YES

Was any supported organization not organized in the United States ("foreign supported organization")? If "Yes" and if you checked 12a or 12b to Part I, answer (b) and (c) below 4ab Did the organization have ultimate control and discretion in deciding whether to make grants to the foreign supported organization? If "Yes," describe in Part VI how the organization had such control and discretion despite being controlled or 4b supervised by or in connection with its supported organizations c. Did the organization support any foreign supported organization that does not have an IRS determination under sections 501 (c)(3) and 509 (a) (1) or (2)? If "Yes," explain in Part VI what controls the organization used to ensure that all support to the foreign supported organization was used exclusively for section 170(c)(2)(8) purposes. **LEFT BLANK**



PETER DASZAK

GAIN-OF-FUNCTION / GAIN-OF-THREAT OUTSOURCED TO WUHAN INSTITUTE OF VIROLOGY AFTER AMERICA BANS IT AS TOO DANGEROUS

2014-2019 Daily Mail: "The US National Institutes of Health (NIH) funded bat-coronavirus research in the Wuhan Institute of Virology in China to the tune of US\$3.7 million. Back in October 2014, the US government had placed a federal moratorium on gain-of-function (GoF) research – altering natural pathogens to make them more deadly and infectious – as a result of rising fears about a possible pandemic caused by an accidental or deliberate release of these genetically engineered monster germs.¹ A portion of \$3.7 million in grants awarded between 2014 and 2019 by the National Institutes of Health (NIH) funded research at the Wuhan Institute of Virology in China. However, not all of that \$3.7 million went to the WIV, and not all of the funding took place under the Obama administration. Approximately \$700,000 of the \$3.7 million total was approved under Donald Trump."

<https://asiatimes.com/2020/04/why-us-outsourced-bat-virus-research-to-wuhan>
<https://www.snopes.com/fact-check/obama-admin-wuhan-lab-grant>

1. The funding was laundered through Daszak's ECOHEALTH ALLIANCE.

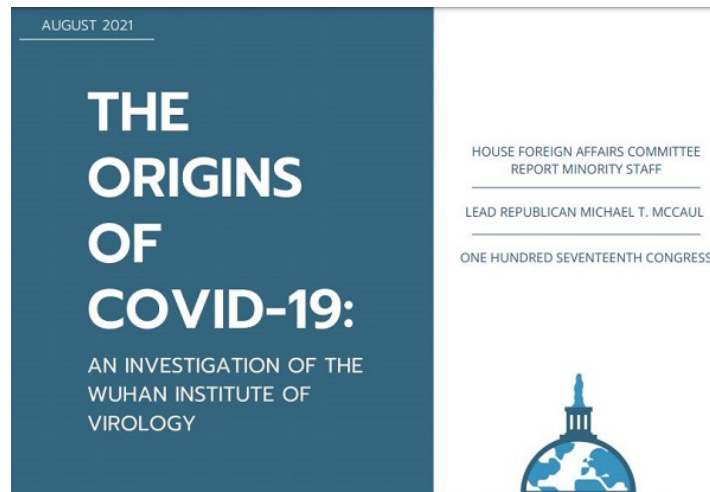
Daszak was one of the first men to find out about the virus because he was expecting a virus to leak and told his assets in China to be on the lookout for it. His story about how he first heard about it is full of contradictions. He told Wired: "On the night after the first Covid-19 post on December 31, 2019, which would be January 1, 2020, Dr. Peter Daszak, a disease ecologist and president of the EcoHealth Alliance, interrupted **Marjorie Pollack's** New Year's Eve dinner [December 31, 2019] to relay details **his Mandarin-speaking staff members** had picked up from China. Early lab work done in the **Wuhan Institute of Virology** (WIV) showed the novel coronavirus behind Covid-19 had 80 percent homology—similarity due to shared ancestry—with the 2003 coronavirus that caused SARS. Daszak wanted the ProMED volunteers to know, he says, because "they are a gold standard for information." He went on: "I got hold of Marjorie Pollack on New Year's Eve [December 31, 2019], and as the champagne was getting warm we realized something really serious was going on in China. We had it from a good source that this was a coronavirus and that it was 20% different to SARS. So we knew that SARS was pretty good at transmitting from person to person; we knew it had a 10% mortality rate. That's a huge red flag. I really knew something was wrong when every single senior person that I was trying to get hold of in

China was busy. I sent a really long text to George Gao, who's head of the CDC. I offered to send a team out there, to come out there and do anything to support them, and I got the shortest response ever from George, which was "Happy New Year." [Wired March 5, 2020](#)

December 31, 2019 the World Health Organization's Country Office in the People's Republic of China picked up a media statement by the Wuhan Municipal Health Commission from their website on cases of 'viral pneumonia' in Wuhan, People's Republic of China. The night after this was January 1, 2020 First Daszak says it came from his **his Mandarin-speaking staff members** then he says he and Dr. Pollack had the same source in China. He was concealing the fact that he was the first to become aware of SARS-CoV-19 from his Bat Lady dupe at the WIV, Shi Zheng Li.

Dr. Shi: "I have been working on the discovery and characterization of novel viruses from bats and other wildlife since 2004. This included the discovery that Chinese horseshoe bats are the natural reservoir of SARSr-CoVs and the likely origin of SARS-CoV. My group then isolated SARSr-CoVs from bats sharing high homology with human SARS-CoV and demonstrated their interspecies transmission risk, largely confirming bats as the source of SARs" (Intercept 352)

[Ira Lipkin lies and tells 9/11 revisionist Spike Lee he was the first to learn of Covid](#)



NO NEWS OF GOP REPORT IN THE NEW YORK TIMES

GOP HOUSE FOREIGN AFFAIRS COMMITTEE MINORITY REPORT FINDINGS: DASZAK'S GoF EXPERIMENTS. NOT TO MAKE VIRUSES MORE DEADLY, BUT TO MAKE THEM TRANSMITTABLE TO NEW HOSTS, AND MORE CONTAGIOUS, CAUSED THE PANDEMIC

"While much of the public debate was initially focused on the Huanan seafood market in Wuhan as the origin of the pandemic, the preponderance of evidence now suggests that the virus leaked from the Wuhan Institute of Virology. Given the WIV's demonstrated history of conducting gain-of-function experiments on coronaviruses, including genetically manipulating viruses specifically to make them infectious to humans in BSL-2 labs, as well as their possession of one of the world's largest of coronaviruses, it is completely plausible that one or more researcher(s) was accidentally infected and carried the virus out of the lab. The evidence outlined above, combined the cover-up conducted CCP authorities, strongly suggest the Wuhan Institute of Virology as the source of the current pandemic.... **After this extensive investigation, we believe it is time to call Peter Daszak to testify before Congress.** There are still many outstanding questions about the type of research he funded at the WIV that only he can answer. In addition, we believe there is legislation Congress can pass that would not only hold those responsible accountable but also help to prevent a future pandemic, including but not limited to:

- Institute a ban on conducting and funding any work that includes gain-of-function research until an international and legally binding standard is set, and only where that standard is verifiably being followed.
- Sanction the Chinese Academy of Sciences and affiliated entities.
- List the Wuhan Institute of Virology and its leadership on the Specially Designated Nationals and Blocked Persons List and apply additional, appropriate secondary sanctions.
- Authorize new sanctions for academic, governmental, and military bioresearch facilities that fail to ensure the appropriate levels of safety and information sharing."

[INITIAL REPORT](#)


CHAPTER 10

VICE PRESIDENT OF ECO-HEALTH DEFECTS



Get to know our scientists! Andrew Huff, Ph.D. Associate Vice President Dr. Andrew Huff began his formal education after two combat tours of duty as an infantryman in Operation Enduring Freedom throughout Central America and in Iraq. After earning a bachelors degree in psychology, and masters degrees in security technologies and geographic information systems (GIS), he was appointed a research fellow at the National Center for Food Protection and Defense (NCFPD) while earning a Ph.D. in Environmental Health specializing in emerging and environmental infectious disease at the University of Minnesota. [ECOHEALTH NEWSLETTER](#)

DRASTIC ON HUFF [Billy Bostickson](#)


**Andrew Huff** •
Improving Health Globally 1d (edited) ***

Unfortunately, Peter's actions and behavior is representative of how science is conducted in 2021. The business of science is just another political football, and has become another form of corporate welfare or government sponsored fraud within higher education. Peter is a master manipulator in science, and he is not the only established scientist playing this game.

Although, his mistakes could be responsible for the deaths of millions.

Peter is a merely the product of the broken and corrupt system that supports research and discovery.


Like · 3 · Reply

**Andrew Huff** •
Improving Health Globally 2d • Edited •

□ □ □ □

More explosive evidence that supports the WIV / EcoHealth / NIH lab leak hypothesis. Definitely not a wet market like Fauci, Daszak, and Chinese authorities claimed.

"...the current study suggests that at least in one case, the trusting structures of science have been abused to obscure sequences relevant to the early spread of SARS-CoV-2 in Wuhan. "

**Dr. Andrew G. Huff**
@AGHuff · Follow


Dr. Peter Daszak told me that he was working with the CIA.


I am blowing the whistle on EcoHealth Alliance.


The truth will get out to everyone. There is A LOT more to the story.

Coming soon in print and other media.

Please retweet.

 **4,535**
+ 0%

 **1,948**
+ 0%

 **115**
+ 0%

Impressions ⓘ
315K
+ 0% from promotion

Engagements ⓘ
49,311
+ 0%

Detail expands ⓘ
31,810
+ 0%

Dr. Andrew Huff filed this request with the Defense Counterintelligence and Security Agency of the United States of America:

My name is Dr. Andrew Huff, and I am working with the House Select Committee on Intelligence with Mr. Ravi Batra, Ravi Batra Law, related to the investigation into the origin of COVID. For the past 2 months I have been under constant surveillance in all forms, my house has been broken into, hard drives have been stolen, electronic eavesdropping equipment has been installed throughout my home, all my electronic devices have been hacked with drones, culminating with being attacked in my house with microwaves from an aircraft. This is due to me revealing that Dr. Peter Daszak of EcoHealth Alliance stated to me that he was working with the CIA. [SOURCE MUCKROCK](#)

CHAPTER 11

BIDEN REDACTED REPORT

The IC [Who is the Intelligence Community?] assesses that SARS-CoV-2, the virus that causes COVID-19, probably emerged and infected humans through an initial small-scale exposure that occurred no later than November 2019 with the first known cluster of COVID-19 cases arising in Wuhan, China in December 2019. In addition, the IC was able to reach broad agreement on several other key issues. We judge the virus was not developed as a biological weapon. Most agencies also assess with low confidence that SARS-CoV-2 probably was not genetically engineered; however, two agencies believe there was not sufficient evidence to make an assessment either way. Finally, the IC assesses China's officials did not have foreknowledge of the virus before the initial outbreak of COVID-19 emerged. After examining all available intelligence reporting and other information, though, the IC remains divided on the most likely origin of COVID-19. All agencies assess that two hypotheses are plausible: natural exposure to an infected animal and a laboratory-associated incident. Four IC elements and the National Intelligence Council assess with low confidence that the initial SARS-CoV-2 infection was most likely caused by natural exposure to an animal infected with it or a close progenitor virus—a virus that probably would be more than 99 percent similar to SARS-CoV-2. These analysts give weight to China's officials' lack of foreknowledge, the numerous vectors for natural exposure, and other factors. One IC element assesses with moderate confidence that the first human infection with SARS-CoV-2 most likely was the result of a laboratory-associated incident, probably involving experimentation, animal handling, or sampling by the Wuhan Institute of Virology. These analysts give weight to the inherently risky nature of work on coronaviruses.

"The IC assesses that SARS-CoV-2, the virus that causes COVID-19, probably emerged and infected humans through an initial small-scale exposure" if it started at the Wuhan Market it would have been large scale "that occurred no later than November 2019 with the first known cluster of COVID-19 cases arising in Wuhan, China in December 2019. In addition, the IC was able to reach broad agreement on several other key issues. We judge the virus was not developed as a biological weapon. [If it was why are the Chinese vaccines ineffective?] Most agencies also assess with low confidence that SARS-CoV-2 probably was not genetically engineered; however, two agencies believe there was not sufficient evidence to make an assessment either way. Finally, the IC assesses China's officials did not have foreknowledge of the virus before the initial outbreak of COVID-19 emerged." Unless we know which Agency made each assessment the information is meaningless.

After examining all available intelligence reporting and other information, though, the IC remains divided on the most likely origin of COVID-19. All agencies assess that two hypotheses are plausible: natural exposure to an infected animal and a laboratory-associated incident. Four IC elements and the National Intelligence Council assess with low confidence that the initial SARS-CoV-2 infection was most likely caused by natural exposure to an animal infected with it or a close progenitor virus—a virus that probably would be more than 99 percent similar to SARS-CoV-2. These analysts give weight to China's officials' lack of foreknowledge, the numerous vectors for natural exposure, and other factors. **One IC element assesses with moderate confidence that the first human infection with SARS-CoV-2 most likely was the result of a laboratory-associated incident, probably involving experimentation, animal handling, or sampling by the Wuhan Institute of Virology. These analysts give weight to the inherently risky nature of work on coronaviruses.** Unless we know which Agency made each assessment the information is meaningless.

Analysts at three IC elements remain unable to coalesce around either explanation without additional information, with some analysts favoring natural origin, others a laboratory origin, and some seeing the hypotheses as equally likely. Variations in analytic views largely stem from differences in how agencies weigh intelligence reporting and scientific publications, and intelligence and scientific gaps. The IC judges they will be unable to provide a more definitive explanation for the origin of COVID-19 unless new information allows them to determine the specific pathway for initial natural contact with an animal or to determine that a laboratory in Wuhan was handling SARS-CoV-2 or a close progenitor virus before COVID-19 emerged. The IC—and the global scientific community—lacks clinical samples or a complete understanding of epidemiological data from the earliest COVID-19 cases. If we obtain information on the earliest cases that identified a location of interest or occupational exposure, it may alter our evaluation of hypotheses. China's cooperation most likely would be needed to reach a conclusive assessment of the origins of COVID-19. Beijing, however, continues to hinder the global investigation, resist sharing information and blame other countries, including the United States. These actions reflect, in part, China's government's own uncertainty about where an investigation could lead as well as its frustration the international community is using the issue to exert political pressure on China.

CHAPTER 12

AN ACCIDENT TOOK PLACE AT THE WIV

Three unidentified workers from the Wuhan Institute of Virology went to the hospital in November 2019 with flu-like symptoms. WAPO: "In China, people visit the hospital for routine and mild illnesses." However the intelligence came from the French who built the high containment lab at the WIV and was a result of an inquiry to the French about what to do about this accident. How to decontaminate the labs.

DASZAK: I remember specifically asking the Wuhan lab director and the staff about people who got sick, and we repeated that and pushed and asked pretty tough questions around that and they refuted it.

GUPTA: According to the Wuhan Institute of Virology on practices, they would have taken blood samples around that time.

DASZAK: Yes.

GUPTA: Did you get to see those blood samples?

DASZAK: No. No. But we did ask them. We asked them if they do that, they confirmed that they did take sample, that they tested them after the outbreak and that they were negative for COVID.

GUPTA (voice-over): The same missing pathogen database containing thousands of bat coronavirus entries that was taken offline by WIV in September of 2019.

ALINA CHAN, BROAD INSTITUTE: So this is a database that the mission was to collect all the viruses in the wild and use it to help prevent pandemics. So this is a pandemic. So why didn't they share that database with other scientists so they could figure out how

dangerous this virus, where did it come from? [A Chinese news outlet accused her of “filthy behavior and a lack of basic academic ethics,” and readers piled on that she was a “race-traitor,” because of her Chinese ancestry. To scientists and editors “who are directly or indirectly covering up severe research integrity issues surrounding the key SARS-2-like viruses to stop and think. If your actions obscure SARS2 origins, you’re playing a hand in the death of millions of people.”]

GUPTA (on-camera): What is the status of that database now? Have you been able now then as a member of this WHO team or in any capacity to look at that data?

DASZAK: No.

GUPTA: That sounds concerning, Peter, if it is as serious and we're trying to be as thorough as possible. Maybe it mounts to nothing but I think the fact that you still haven't seen that database, it's just going to raise a lot of eyebrows as we go forward.

DASZAK: Well, rightly so. I think that, you know, China should be more open about the things that they've not released. But this is where politics comes into and when a country is under attack, and they defend and then scientists are caught in the middle of it. It's really unfortunate.

GUPTA (voice-over): Dr. Shi Zhengli and others at the Wuhan Institute of Virology did not respond to interview requests for this documentary.



"These analysts also note that China's investigations into the pandemic's origin might not uncover evidence of a laboratory-associated incident if it involved only a small number of researchers who did not acknowledge or have knowledge of a potential infection. Updated Assessment on COVID-19 Origins"

CHAPTER 13

CHICOM PROP IS ABSURD



Is the so-called “respiratory disease” or “white lung disease” of unknown cause that broke out in the United States in the second half of 2019 as new coronary pneumonia? What kind of research is being carried out in Fort Detrick and other biological laboratories in the United States? Is it related to coronavirus? How are the security measures implemented? Is it related to the origin of the global new crown epidemic? These are all questions that should be answered in the tracing of the new crown, but the US government has been covering up. In order to use the epidemic to achieve political goals, the US government suppressed scientists and suppressed professional opinions. In particular, scientists who deny the “laboratory leak theory” are subjected to cyber violence and harassment, not only affecting their normal work, but even facing personal threats.

Beijing won't accept the W.H.O's proposed second phase investigation into the origins of the Covid-19 pandemic, accusing it of “arrogance” and a “disrespect for common sense” with its return to the “lab leak” theory. Zeng Yixin, deputy minister of the National Health Commission, said he was “very surprised” when he first read about the proposed study “because it places the hypothesis that ‘China’s breach of laboratory protocols caused the virus to leak’ as one of the research priorities.” Zeng said none of the staff or postgraduates at the Wuhan Institute of Virology – at the centre of the lab leak claims – had been infected with the new coronavirus

and the lab had not conducted any gain-of-function studies. Fauci approved Daszak re-purposing NIH grants to the WIV so these experiments could go forward, assuming his Deputy, Erik Stemmy, apprised him of them. [South China Morning Post](#)

GOP ORIGINS REPORT: "Therefore, it is reasonable to conclude, based on the WIV's extensive sample library and history of genetically manipulating coronaviruses, that in early September, one or more researchers became infected with SARS-CoV-2 in the lab and carried it out into the city. Based on the WIV's publications, researchers could have been exposed while experimenting with a natural virus collected from the wild or infected with a virus they genetically manipulated. Those researchers likely traveled to and from the WIV via the Wuhan metro or via the shuttle service, providing a vector for the virus to spread. This corresponds with the first signs of a growing wave of ill people in Wuhan centered around the WIV's Wuchang facility."

FAUCI TRUSTS THE CHINESE COMMUNIST PARTY?

Doctor Anthony Fauci states we can't rely on the three scientists falling ill, intell, until China produces the scientists medical records, as if this were a real possibility. China is a "socialist" slave-state where 43% of the population, earns \$150-a-month and a country that [routinely launches cyber-attacks against the U.S.](#) The Chinese insist that Covid-19 didn't originate in Wuhan so there will never be any medical records. CCP spokeswoman Hua Chunying: "I'd like to stress that if the United States truly respects facts, it should open the biological lab at Fort Detrick, Maryland, give more transparency to issues like its 200-plus overseas bio-labs, invite WHO experts to conduct origin-tracing in the United States, and respond to the concerns from the international community with real actions."

JULY 2021: FAUCI WANTS TO REVIVE DASZAK'S PREDICT PROGRAM THAT FAILED TO PREDICT THE PANDEMIC

"The idea is to make "prototype" vaccines to protect against viruses from about 20 families that might spark a new pandemic. Using research tools that proved successful for Covid-19, researchers would uncover the molecular structure of each virus, learn where antibodies must strike it, and how to prod the body into making exactly those antibodies. It would cost "a few billion dollars" a year, take five years for the first crop of results and engage a huge cadre of scientists, he said." There has never been a vaccine produced by GoF / GoT experiments either before and outbreak or after one. It is junk science. [No Mention of GoF experiments in new PREDICT plan](#)

CHAPTER 14

DASZAK IS A MOLE WHO INFILTRATED FAUCI, BARIC AND LI'S SCIENTIFIC CIRCLES

Daszak: "We have obtained a letter of support from Dr Ralph Baric, who is keen to collaborate with us initially to infect his humanized mouse model with our bat SL-CoV that uses ACE2, and subsequently to use other CoVs we identify (see Dr Ralph Baric, Letter of Support) Intercept 125. In **October 2014** President Obama banned Gain-of-Threat experiments in the USA. Obama feared a global pandemic if one of the nano particle-sized viruses escaped via a leak or in an infected human or animal. Daszak was one step ahead of Obama, with help from the NIH's Fauci, Daszak had already outsourced the experiments to the WIV. Again, Gain-of-Threat experiments, called "Gain-of-Function" experiments, utilize genetic engineering to make a virus hundreds of times more transmittable than the virus nature created. GoF is also used to expand the number of hosts the virus can infect. SARS-CoV-2 was not designed to mutate rapidly making it difficult for vaccines to be developed that would work on every variant.¹ But it is in so many human hosts that it does just that: e. g. "About half of adults infected in a June 2021 outbreak of the Delta variant of Covid-19 in Israel were fully inoculated with the Pfizer Inc. vaccine, prompting the government to reimpose an indoor mask requirement and other measures to contain the highly transmissible strain." However the NYT reported: "The vaccines made by Pfizer-BioNTech and Moderna set off a persistent immune reaction in the body that may protect against the coronavirus for years, scientists reported. The findings add to growing evidence that most people immunized with the mRNA vaccines may not need boosters, **so long as the virus and its variants do not evolve much beyond their current forms — which is not guaranteed.**" The paradigm for many was that Israel is the most vaccinated country in the world, that vaccinated people rarely become infected, that even more rarely do they become severely ill and that basically, with very few precautions in place, the population was very close to herd immunity. The problem was that what was true for the original virus "did not necessarily hold true for future variants coupled with waning immunity."

1. "Variant" is a mutation. That's a word no one likes to use.

Despite Obama's Executive Order, made against the wishes of NIH head Fauci, Dr. Daszak continued to "re-purpose" part of his NIH / NIAID / USAID (CIA lite) grant money to the WIV where no such ban existed, so it could continue the GoT experiments. Why was Daszak gung-ho on seeing gain-of-threat experiments continue? Daszak's cover is liberal-Democrat but he is really a Chinese agent-of-influence. [Daszak's organization, Eco-Health Alliance, was first described as a foreign entity.](#) Daszak is a Fascist, a reincarnation of his Fascist father Bohdan Daszak, but this time around, an Eco-Fascist.

CHAPTER 15

CHINESE-AGENT-OF-INFLUENCE PETER DASZAK TWEETS





MARION KOOPMANS

Not only did Daszak orchestrate the pandemic, but he, along with Dr. Marion Koopmans, orchestrated the coverup. Daszak was the most visible presence in the [bogus W.H.O. investigation](#) that blamed the pandemic on imported frozen meat.

Daszak: "What possible infection sources in Huanan market? Could have been introduced by a person, or a product (e.g. frozen farmed wildlife INCLUDING SPECIES SUSCEPTIBLE TO COVID)..Vendors were trading wildlife products..frozen. From farms within the country. On future work amidst [Chinese] political sensitivities: "I stand resolute against the political attacks that we see every day. [In Wuhan] we met scientists who are ready, willing & able to collaborate. I'm looking forward to digging deeper & tracing back the origins of this virus....What we found is evidence of a way the virus could have emerged from rural China into a big city like Wuhan... at the end of the report, both the China team of experts & the WHO experts all felt this was the most likely pathway that the virus took. The WHO team examined lab work of a number of researchers in Wuhan & found "no evidence at all that any of the labs in China were working on this virus prior to the outbreak...Did they have viruses that were potential ancestor of SARS-CoV-2? Again, no evidence of that. Attempts to re-engage with China may not be the worst thing. The Trump administration taught us that the United States' most effective way of destabilizing China is to destabilize itself. That this is a foolish exercise should be self-evident. We need better options."



The CGTN report quoted Daszak as saying "there is a huge amount of evidence that these viruses repeatedly emerge into people from wild animals in rural areas through things like hunting and eating wildlife" and that it was "almost impossible for it to have come out of a lab." [The Polygraph 2021 in Review: China Led in Global Disinformation On COVID-19 Pandemic](#)

HAVING DASZAK AS A W.H.O INVESTIGATOR WAS LIKE HAVING AL CAPONE SIT ON ON THE CHICAGO CRIME COMMISSION.

The Chinese blamed the pandemic on frozen meat imported from Barcelona, Spain. Daszak blamed it on frozen meat from China. Daszak was also behind [this letter in the Lancet](#), a highly respected medical journal, which read in part "Conspiracy theories do nothing but create fear, rumours, and prejudice that jeopardise our global collaboration in the fight against this virus." [Daszak has recused himself from Lancet Covid-19 Commission after hearing he was going to be fired!](#)

DASZAK TELLS GUPTA HIS DEFINITION OF CONSPRACY THEORY INVOLVED BIO-WARFARE, NOT A LAB LEAK

GUPTA: The thing I think that struck me it was so early. How were you so certain at that point to go ahead and label anything that was not a natural origin a conspiracy theory?

DASZAK: Well, because the theory at the time was this is a bio- engineered virus.

GUPTA: So this was not in any way to take off the possibility that this could have still leaked from a lab even if it had not been bio-engineered?

DASZAK: That was not what was being said at the time. What was being said at the time is this is a bio-engineered virus that had been released by Chinese scientists.

CHAPTER 16

FAUCI'S INVOLVEMENT IN CREATING THE PANDEMIC

Fox's Jesse Watters: "So now he's in trouble. Now you're going for the kill shot. The kill shot with an ambush, deadly. Because he doesn't see it coming. This is when you say. 'Dr. Fauci, you funded risky research at a sloppy Chinese lab. The same lab that sprung this pandemic on the world. You know why people don't trust you, don't you?'"





DR. ANTHONY FAUCI LIED ABOUT GAIN-OF-THREAT HIH FUNDING

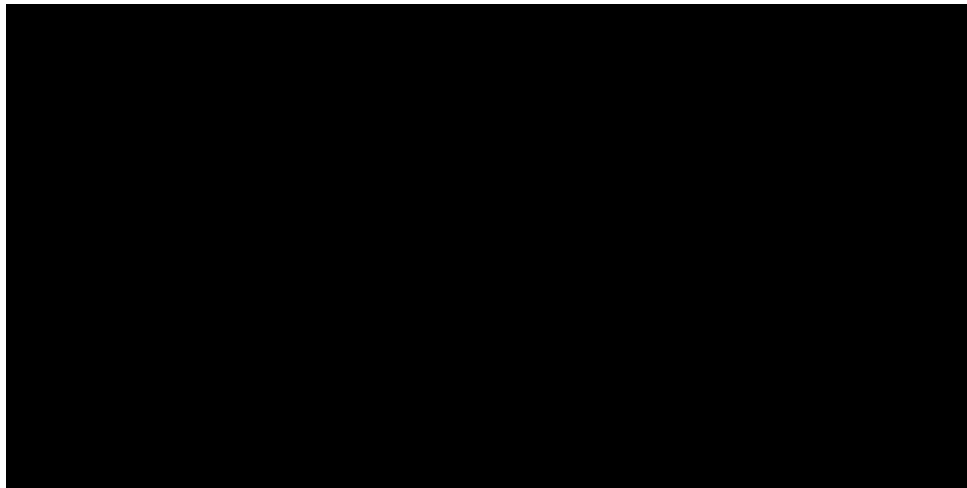
In 1968, Dr. Anthony Fauci came to NIH as a clinical associate in the NIAID Laboratory of Clinical Investigation. In 1980, he was appointed chief of the Laboratory of Immunoregulation, a position he still holds. Dr. Fauci became director of NIAID in 1984 a position he still holds earning him the nickname **J. Edgar Fauci** for his long tenures. In when Fauci earned \$417,608, making him the highest-paid federal employee at the time. NIH is the largest source of funding for medical research in the world National Institute of Health (NIH) National Institute of Allergy and Infectious Diseases (NIAID) goal is "To support a discrete, specified, circumscribed project to be performed by the named investigator(s) in an area representing his specific interest and competencies" Research Project (R01) Project 5R01AI110964-04 Application 9320765 Study Section: Clinical Research and Field Studies of Infectious Diseases Study Section (CRFS) **Program Officer Erik J Stemmy** approved Daszak's grants.

Dr. Erik Joseph Stemmy, PhD erik.stemmy@nih.gov BG 560 1FL RM 8E18 5601 FISHERS LN ROCKVILLE MD 20852 Mail Stop: 9825 Phone: 240-627-3380 NIAID (National Institute of Allergy and Infectious Diseases) VIRAL RESPIRATORY DISEASES SECTION (HNM563)



FIRE FAUCI AND REPLACE HIM WITH FORMER FDA HEAD Dr. SCOTT GOTTLIEB

GoF/GoT research out-sourced to China was approved by Dr. Erik Joseph Stemmy, PhD, who worked under NIH / NIAID head Anthony Fauci, and was in charge of vetting Viral Respiratory Diseases Section grants. Obama had issued an Executive Order banning these procedures and these two highly erudite men knew farming the experiments out to China was a way of circumventing the moratorium. Violation of an Executive Order by a Federal Government employee can be a crime but in most instances, it's the same penalty any employee suffers when he defies the boss: a reprimand, a demotion, firing. If you are a civil servant the head of your Department will bring administrative charges against you (as prescribed by law) based on the severity of the offense. But here's the catch "The Obama decree prevented the start of new programs, although the program started in 2014 before the Obamian moratorium, via the EcoHealth Alliance, had already secured \$ 3.7 million to the Chinese researchers in Wuhan to continue deepening their studies of "epidemiological surveillance" that included the work to gain function until 2019. Part of the research was therefore carried out at the Wuhan Institute of Virology, outside the reach or control of the North American authorities, as Daszak clearly reveals in the interview we discussed. in the beginning. That is, after the deliberation process, the moratorium had been lifted in December 2017 by the Trump administration, but the previous situation of complete freedom was not returned for these investigations. What was done was to create a governmental control mechanism, a panel of experts called P3CO, to which the NIH should refer any project that includes profit of function or similar risks, to be scrutinized before the corresponding funding is granted. Quite simply, when Fauci sent the second phase of the coronavirus gain-of-function project through the EcoHealth Alliance - another \$ 3.7 million for another five years, 2019-2024, for the WIV - he managed to avoid that it be raised to the consideration of the panel of experts. He managed not to notify the panel, and when he was asked to account for it much later, he argued that he did not do so because the work did not involve any biosafety danger. Extramural In a recent NBC News Poll, just 40 percent of respondents said they trusted Dr. Fauci, down from 60 percent in April 2020. NBC

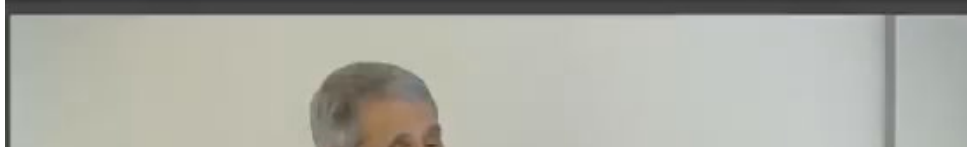


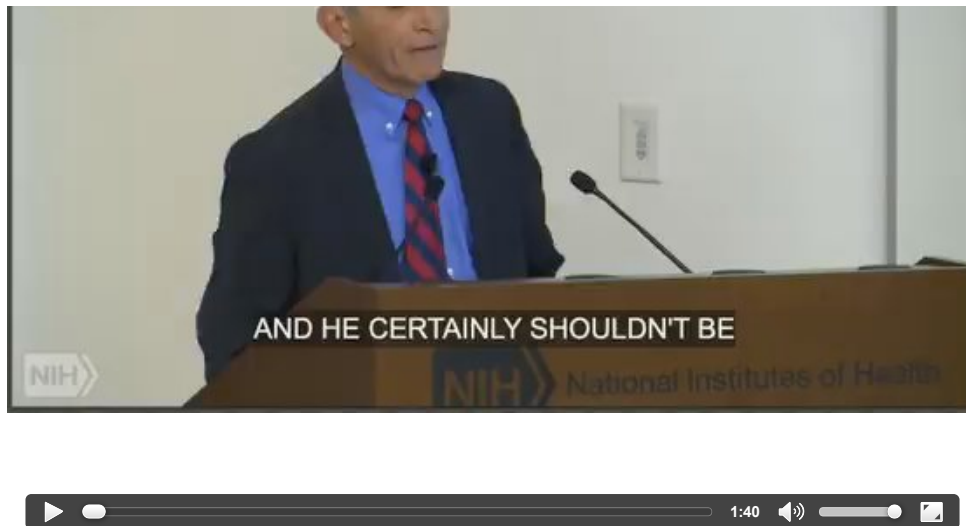
When questioned by a U. S. Senator Rand Paul*, Dr. Fauci said he didn't know what types of experiments were being conducted at the WIV, although in order to get grant money the recipient has to specify what the money is for as we can see from the document reproduced below entitled "The Possibility that the COVID-19 Virus had a Wuhan Laboratory Origin by Peter Daszak." Doc Fauci's latest in the [NYT](#): "There is this so-called intelligence that three members of the human lab were ill, requiring hospitalization. And I really wonder what the strength of that intelligence is, what the confidence in it is. It certainly has gotten bantered around. And I have said that if the intelligence is firm and real, then you should **make sure we find out what the health records of those sick people are**. But if it's very weak, flimsy intelligence, then there's nothing there. I always keep an open mind. I feel, as do the overwhelming majority of scientists who have knowledge of virology and knowledge of evolutionary biology, that the most likely explanation for this is a natural leap from an animal reservoir to a human." Does Fauci really expect China to give us those records? Of course the Chinese will deny they exist or falsify them. They don't want to take the blame for the pandemic.

*Rand (named after the South African currency) is the son of [target="_blank">Ron Paul](#) a crypto-Nazi connected with the now defunct Liberty Lobby. It is a shame he is Fauci's #1 foe or I would work with him as I did with Congressman Henry Gonzalez and Senator Lowell Schweiker, both deceased. Ron Paul edited this statement to make it seem vaccines don't work "We know that the two doses of the vaccine offer very limited protection, if any," is where Paul's quotation ends. "The three doses, with the booster, they offer reasonable protection against hospitalization and deaths. Against deaths, I think very good, and less protection against infection."



NIAID Advisory Council Meeting - January 2018





Fauci: "We still haven't found the natural source of Ebola. And that's been since 1976." The CDC: "African fruit bats are likely involved in the spread of Ebola virus and may even be the source animal (reservoir host). Scientists continue to search for conclusive evidence of the bat's role in transmission of Ebola. The most recent Ebola virus to be detected (August 2018), Bombali virus, was identified in samples from bats collected in Sierra Leone." [Center For Disease Control](#) But there was no Democratic Republic of Congo Institute for the Study of Ebola viruses where it first broke out and Ebola killed 11,310 not 4 million. The search for the Ebola intermediate species revealed: "Combining results on Non Human Primates from our [4,649](#) samples and previous studies, it is clear that Ebola virus antibodies are not widespread among NHP which confirms that NHPs are not reservoir species and that if Ebola virus infection in NHPs occurs, few animals survive." During the W.H.O visit, the team reviewed sampling from extensive PCR tests of livestock and poultry from 31 Chinese provinces and 50,000 samples of the wild animals covering 300 different species, but not a single one was found to be infected with SARS-CoV2. <https://healthpolicy-watch.news/who-experts-unable-to-find-missing-link-in-sars-cov2-transmission-in-china/>

Like Daszak, Fauci often uses the term "conspiracy theory" for things he disagrees with "And any thought of that is total conspiracy theory and total flight of fantasy." There was no conspiracy between Shi, Daszak and Baric. Daszak made Shi and Baric unwitting participants.

Dr. FAUCI, WHO APPROVED DASZAK'S GRANTS, WANTS ANOTHER INVESTIGATION BECAUSE IF HE SAID HE DIDN'T SUSPICION WOULD FALL ON HIM



"No actually. I am not convinced about that [the origins of Vovid19]. I think we should continue to investigate what went on in China until we continue to find out to the best of our ability what happened. Certainly, the people who investigated it say it likely was the emergence from an animal reservoir that then infected individuals, **but it could have been something else**, and we need to find that out. So, you know, that's the reason why I said I'm perfectly in favor of any investigation that looks into the origin of the virus." A day after Fauci made this statement *The Wall Street Journal* elaborated on a report included [on this webpage](#). "Three researchers from China's Wuhan Institute of Virology became sick enough in November 2019 that they sought hospital care, according to a previously undisclosed U.S. intelligence report that could add weight to growing calls for a fuller probe of whether the Covid-19 virus may have escaped from the laboratory." Dr. Erik Joseph

Stemmy, who also approved Daszak's grants, should also be held accountable for his actions.

Fauci: "We're not talking about the Communist Chinese party. We're not talking about the Chinese military. We're talking about scientists that we've had relationships [with] for years. The Wuhan lab is a very large lab, to the tune of hundreds of millions if not billions of dollars — the grant that we're talking about was \$600,000 over five years. I can't guarantee everything that's going on in the Wuhan lab, we can't do that, but it is our obligation as scientists and public health individuals to study the animal-human interface....A lot of what you're seeing as attacks on me, quite frankly, are attacks on science because all of the things that I have spoken about consistently from the very beginning, have been fundamentally based on science ... People want to fire me or put me in jail for what I've done — namely, follow the science. The most likely origin is a natural origin from an animal reservoir to human. However, we have not ruled out the possibility that there could have been a leak from the lab. I haven't changed my mind."

Dr. Fauci: "Yeah, 20 years ago, people would ask me the same question.[What are you watching for next?] And if you go back over the records, which is easy to do, you would see that I consistently gave the same answer. And that is the emergence of a new virus, a respiratory borne virus that would jump species from an animal host to a human that would have two characteristics. One, it would be highly efficient in transmissibility through the respiratory route. And two, it would have a very high degree of capability of morbidity and mortality for the human population. And unfortunately, we're living through my worst nightmare." This is an false equivalence: SARS surfaced 19 years ago yet it was quickly contained. SARS-CoV-19 still is deadly - June 2021 - ten thousand a week dead. [NYT](#)





REP. RAND PAUL (R), KENTUCKY: : Dr. Fauci, knowing that it is a crime to lie to Congress do you wish to retract your statement of May 11, where you claimed that the NIH never funded gain-of-function research in Wuhan?

DR. ANTHONY FAUCI, DIRECTOR OF NIH: Senator Paul I have never lied Senator Paul, I have never lied before the Congress and I do not retract that statement. This paper that you are referring to was judged by qualified staff up and down the chain as not being gain-of-function. And if anybody is lying here --Senator, it is you. Senator Paul, I have never lied before the Congress.

PAUL: But (ph) it could have been. So you're saying if you take an animal virus and you increase transmissibility to humans -- you're saying that's not gain-of-function?

FAUCI: What was -- let me finish. Yes, that is correct. And Senator Paul, you do not know what you are talking about, quite frankly. And I want to say that officially. You do not know what you are talking about.

PAUL: This is your definition that you guys wrote. It says that scientific research that increases the transmissibility among -- the transmissibility among animals is gain-of-function. They took animal viruses that only occur in animals and they increased their transmissibility to humans. How you can say that is not gain-of-function --

FAUCI: It is not.

PAUL: -- it's a dance and you're dancing around this because you're trying to obscure responsibility for 4 million dying around the world from a pandemic.

FAUCI: I have to -- well, now you're getting into something. **If the point that you are making is that the grant that was funded as a subaward from EcoHealth to Wuhan created SARS-CoV-2, that's where you are getting, let me finish.** PAUL: We don't know if it did come from the lab, but all the evidence is pointing that it came from the lab. And there will be responsibility for those who funded the lab, including yourself.

FAUCI: -- I totally resent the lie that you are now propagating, Senator, because if you look at the viruses that were used in the experiments that were given in the annual reports that were published in the literature it is molecularly impossible.

PAUL: No one's saying those viruses caused it.

FAUCI: It -- it is -- it is molecularly --

PAUL: No one is alleging that those viruses caused the pandemic. What we're alleging is that gain-of-function research was going on in that lab and NIH funded it.

FAUCI: Can I answer the question?

PAUL: This is your definition that you guys wrote. It says that scientific research that increases the transmissibility among -- the transmissibility among animals is gain-of-function. They took animal viruses that only occur in animals and they increased their transmissibility to humans. How you can say that is not gain-of-function --

FAUCI: It is not.

PAUL: -- it's a dance and you're dancing around this because you're trying to obscure responsibility for 4 million dying around the world --from a pandemic. And there will be responsibility for those who funded the lab, including yourself.

FAUCI PROPONENT OF GoF / GoT OPPOSES GoF / BAN IN WASHINGTON POST AND DEFENDS GAIN-OF-FUNCTION / GAIN-OF-THREAT EXPERIMENTS

"The question is whether benefits of such research outweigh risks. The answer is not simple. A highly pathogenic bird flu virus transmissible in humans could arise in ways not predicted by laboratory studies. And it is not clear whether this laboratory virus would behave in humans as it does in ferrets. Nonetheless, new data provide valuable insights that can inform influenza preparedness and help delineate the principles of virus transmission between species. **Given these uncertainties, important information and insights can come from generating a potentially dangerous virus in the laboratory.** While the World Health Organization and the Centers for Disease Control (CDC) and Prevention provide excellent public health surveillance for novel influenza strains, influenza outbreaks still occur suddenly and in unexpected places. The recent H1N1 pandemic exemplifies the problem: In 2009, a new influenza virus emerged. It was shown to

have originated from an animal reservoir, and it spread so rapidly that it strained the pharmaceutical industry's capacity to prepare vaccines fast enough to blunt its spread. We do not fully understand the underlying factors that allow influenza viruses to be transmitted efficiently in humans after they emerge from different species. The ferret transmission studies were intended in part to fill these important gaps in knowledge. Understanding the biology of influenza virus transmission has implications for outbreak prediction, prevention and treatment. **In defining the mutations required for mammalian transmission, public health officials are provided with genetic signatures that, like fingerprints, could help scientists more readily identify newly emergent, potentially harmful viruses, track their spread and detect threatening outbreaks.** The ability to identify such viruses even a few months faster than by conventional surveillance provides critical time to slow or stop an outbreak. For example, the CDC implements public health protective measures and stockpiles antiviral drugs. Identifying threatening viruses can also facilitate the early stages of manufacturing vaccines that protect against such a virus in advance of an outbreak. In addition, determining the molecular Achilles' heel of these viruses can allow scientists to identify novel antiviral drug targets that could be used to prevent infection in those at risk or to better treat those who become infected. **Decades of experience tells us that disseminating information gained through biomedical research to legitimate scientists and health officials provides a critical foundation for generating appropriate countermeasures and, ultimately, protecting the public health."**
https://www.washingtonpost.com/opinions/a-flu-virus-risk-worth-taking/2011/12/30/gIqAM9sNRP_story.html

GO BACK

BENEFITS AND RISKS OF INFLUENZA RESEARCH: LESSONS LEARNED ANTHONY S. FAUCI, FRANCIS S. COLLINS

"One of the goals of pandemic influenza research is to recognize and anticipate how viruses are evolving in the wild toward a phenotype that is dangerous to humans, thereby staying one step ahead of potential pandemics. In this regard, compelling research questions relevant to global health and pandemic preparedness include determining whether highly pathogenic viruses, such as H5N1, have the ability to mutate and/or reassort with another influenza virus to become readily transmissible by the airborne route among humans. If so,

- (i) what is the likelihood that such mutations or reassortments will happen in nature?
- (ii) Is there a genetic signature of such a virus that might be helpful in surveillance?
- (iii) Would such a virus be highly pathogenic for humans?
- (iv), would such a virus be sensitive to currently available antiviral drugs and vaccines, or would new ones be necessary?

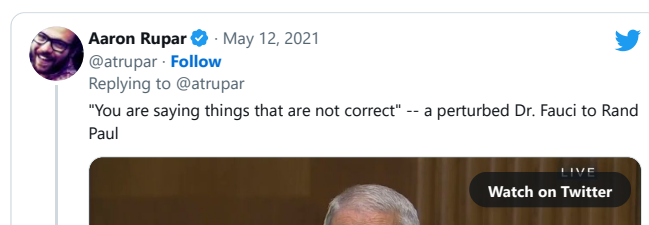
"Within this context, global attention has been paid recently to two NIH-funded studies of H5N1 transmissibility and pathogenesis in ferrets. In those studies, H5N1 viruses were made transmissible via respiratory droplets among ferrets by engineering the virus; well-described and published protocols including reverse genetics, reassortment, and passaging of viruses in mammals were used. Manuscripts describing the studies have generated an unprecedented degree of discussion, concern, and disagreement among scientists, as well as the public, regarding whether the experiments should have been performed in the first place and whether they should be published in their entirety. **Major sources of concern have been that the results might be used by bioterrorists to harm the public or that the virus might accidentally escape and cause a pandemic."**

"However, whenever one deliberately manipulates a virus or a microbe, it is always possible, at least theoretically, that the research results could be used by bioterrorists to intentionally cause harm, or that an accidental release of a pathogen from a laboratory could inadvertently cause harm. Such research is referred to as "dual-use research," as the research potentially has both positive and negative applications. A particular subset of dual-use research is referred to as "dual-use research of concern" or DURC. DURC is defined as life sciences research that, on the basis of current understanding, can be reasonably anticipated to provide knowledge, information, products, or technologies that can be directly misapplied to pose a significant threat with broad potential consequences to public health and safety, agricultural crops and other plants, animals, the environment, materiel, or national security. If a particular experiment is identified as DURC, that designation does not inherently mean that such research should be prohibited or not widely published. However, it does call for us to balance carefully the benefit of the research to public health, the biosafety and biosecurity conditions under which the research is conducted, and the potential risk that the knowledge gained from such research may fall into the hands of individuals with ill intent. Research that could enhance the transmissibility of H5N1 viruses clearly is DURC."

"In this regard, the question of whether to publish the two **H5N1** studies in ferrets has been intensively discussed by an independent federal advisory committee known as the National Science Advisory Board for Biosecurity (NSABB). **On the basis of their recommendations and other evaluations, the U.S. government agreed that the research is important for the public health and should be published.** However, important lessons were learned along the way and, appropriately, triggered an examination of our approach concerning the conduct, oversight, and communication of DURC. In this regard, the U.S. government announced on **March 29, 2012** the U.S. Government Policy for Oversight of Life Sciences Dual Use Research of Concern. This policy document outlines, for federal departments and agencies that conduct or fund life sciences research, steps to determine whether projects fall under the definition of DURC, to assess the risks and benefits of these projects, to review them regularly, and to develop risk mitigation plans. In the process of weighing the potential risks and benefits of publishing these two manuscripts, it also became clear that, when possible, it is critical to identify research with DURC potential before the initiation of the project and, certainly, before the results are submitted for publication. Such monitoring in the case of NIH-funded research requires the concerted effort of all involved, including scientists applying for or in receipt of NIH funding and NIH program officials. Additional guidelines will be needed as well to assist biosafety committees in evaluating DURC at the institutions where the research is conducted.

<https://science.sciencemag.org/content/336/6088/1522.full> 22 Jun 2012

FAUCI SUPPORTED GAIN-OF-FUNCTION / GAIN-OF-THREAT





Aaron Rupar
@atrupar · Follow

"We have not funded gain of function research on this virus in the Wuhan Institute of Virology. No matter how many times you say it, it didn't happen." -- Fauci to Rand Paul



THE LANCET QUESTIONS DASZAK'S OBJECTIVITY "ADDENDUM: COMPETING INTERESTS AND THE ORIGINS OF SARS-COV-2"

Editors of *The Lancet* Published: June 21, 2021 : [Digital Object Identifier](#)

In February, 2020, 27 public health experts co-authored a Correspondence in *The Lancet* ("Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19"), supporting health professionals and physicians in China during the early stages of the COVID-19 pandemic. In this letter, the authors declared no competing interests. Some readers have questioned the validity of this disclosure, particularly as it relates to one of the authors, Peter Daszak. In line with guidance from the International Committee of Medical Journal Editors, medical journals ask authors to report financial and non-financial relationships that may be relevant to interpreting the content of their manuscript. There may be differences in opinion as to what constitutes a competing interest. Transparent reporting allows readers to make judgments about these interests. Readers, in turn, have their own interests that could influence their evaluation of the work in question. With these facts in mind, *The Lancet* invited the 27 authors of the letter to re-evaluate their competing interests. Peter Daszak has expanded on his disclosure statements for three pieces relating to COVID-19 that he co-authored or contributed to in *The Lancet*—the February, 2020, Correspondence, as well as a Commission Statement and a Comment for the *Lancet* COVID-19 Commission. The updated disclosure statement from Peter Daszak is:

"Peter Daszak's remuneration is paid solely in the form of a salary from EcoHealth Alliance, a 501(c)(3) non-profit organisation. EcoHealth Alliance's mission is to develop science-based solutions to prevent pandemics and promote conservation. Funding for this work comes from a range of US Government funding agencies and non-governmental sources. All past and current funders are listed publicly, and full financial accounts are filed annually and published. EcoHealth Alliance's work in China was previously funded by the **US National Institutes of Health (NIH)** and the United States Agency for International Development (USAID). Neither Peter Daszak nor EcoHealth Alliance have received funding from the People's Republic of China. Peter Daszak joined the WHO–China joint global study on the animal origins of SARS-CoV-2 towards the end of 2020 and is currently a member. As per WHO rules, this work is undertaken as an independent expert in a private capacity, not as an EcoHealth Alliance staff member. The work conducted by this study was published in March, 2021. EcoHealth Alliance's work in China includes collaboration with a range of universities and governmental health and environmental science organisations, all of which are listed in prior publications, three of which received funding from US federal agencies as part of EcoHealth Alliance grants or cooperative agreements, as publicly reported by NIH. **EcoHealth Alliance's work in China is currently unfunded.** All federally funded subcontractees are assessed and approved by the respective US federal agencies in advance and all funding sources are acknowledged in scientific publications as appropriate. EcoHealth Alliance's work in China involves assessing the risk of viral spillover across the wildlife–livestock–human interface, and includes behavioural and serological surveys of people, and ecological and virological analyses of animals. This work includes the identification of viral sequences in bat samples, and has resulted in the isolation of three bat SARS-related coronaviruses that are now used as reagents to test therapeutics and vaccines. **It also includes the production of a small number of recombinant bat coronaviruses to analyse cell entry and other characteristics of bat coronaviruses for which only the genetic sequences are available. NIH reviewed the planned recombinant virus work and deemed it does not meet the criteria that would warrant further specific review by its Potential Pandemic Pathogen Care and Oversight (P3CO) committee.** All of EcoHealth Alliance's work is reviewed and approved by appropriate research ethics committees, Institutional Animal Care and Use Committee, **Institutional Review Boards for biomedical research involving human subjects**, P3CO oversight administrators, and biosafety committees, as listed on all relevant publications." [Daszak is saying that Fauci approved the experiments that this researcher believes created SARS-CoV-19 and did not subject the to review by Potential Pandemic Pathogen Care and Oversight (P3CO) committee. No wonder Fauci is a proponent of Zoonotics.]

The names of the P3CO scientists are classified and their approval only applies to USG sponsored projects. "The secrecy of the screening process was the most worrisome part of government oversight of potentially dangerous research, according to Angela Rasmussen, a virologist at University of Saskatchewan's Vaccine and Infectious Disease Organization, who was doing research in the United States at that time. "It's not clear how they decide what's acceptable gain of function and what's not," she said. However, the "star chamber" nature of the process was not its biggest problem, said Richard Ebright, a molecular biologist at Rutgers who has also been one of the most vocal proponents of the lab leak theory, and a longtime advocate of stricter control of research on dangerous pathogens. An even bigger issue, he said,

was that gain-of-function research was simply not being screened in accordance with the policy established by H.H.S., which includes the National Institute of Allergy and Infectious Diseases, run by Dr. Fauci. The ideal solution, he said, would be the creation of an independent body to provide the oversight of dangerous pathogen research, similar to what the Nuclear Regulatory Commission does for studies of radioactive materials.

<https://www.nytimes.com/2021/06/20/science/covid-lab-leak-wuhan.html>



CHAPTER 17

DASZAK PLAYED ON THE BENEFICENT MOTIVATION OF MOST SCIENTISTS WHO CONDUCT GoF / GoT EXPERIMENTS



Why in the devil create a novel virus capable of causing a pandemic? Former *New York Times* journalist Nick Wade: "Ever since virologists gained the tools for manipulating a virus's genes, they have argued they could get ahead of a potential pandemic by exploring how close a given animal virus might be to making the jump to humans. And that justified lab experiments in enhancing the ability of dangerous animal viruses to infect people, virologists asserted. With this rationale, they have recreated the 1918 flu virus, shown how the almost extinct polio virus can be synthesized from its published DNA sequence, and introduced a smallpox gene into a related virus. These enhancements of viral capabilities are known as gain-of-function, gain-of-threat, experiments. With coronaviruses, there was particular interest in the **Spike Proteins**, which jut out all around the spherical surface

of the virus and pretty much determine which species of animal it will target. In 2000 Dutch researchers, for instance, earned the gratitude of rodents everywhere by genetically engineering the **Spike Protein** of a mouse coronavirus so that it would attack only cats." Daszak: "Excellent thread debunking another line of argument in Wade's biased, disingenuous, & wildly erroneous piece. So, in just 1 day of Twitter responses, an @NIH statement that they did NOT fund GoF studies at WIV & the Furin cleavage site is NOT a 'smoking gun'. I guess Wade got paid & the conspiracists got their chance to point fingers. Meanwhile, somewhere in a wildlife farm in SE Asia..."

<https://nicholaswade.medium.com/origin-of-covid-following-the-clues>

Using NIH grants and later Daszak's re-purposed grant money, Shi Zheng Li conducted experiments based on a 2005 report by herself and Daszak that proved bat SARS-related CoV (SARSr-CoV) was closely related to human SARS-CoV, implying a bat origin of human SARS. Since then, more bat SARSr-CoV isolates were identified in China. Genome identities of these other bat SARSr-CoVs are as high as 92% to human SARS-CoV, **but their major receptor binding spike proteins cannot use the human virus entry receptor ACE2 cells that line the lungs**. Shi Zheng Li's motivation was to discover which of these viruses would mutate allowing it to enter ACE-2 receptors. Using Gain-of-Threat bio-engineering the scientists at the WIV altered the receptor binding spike so it do just that making it a threat to humans. Shi Zheng Li's rational behind this was an effort to develop a vaccine for this new virus before there was a spillover from bats to an intermediate species and then to human beings or directly from bats to human beings **but the road to Hell is paved with good intentions**. Nick Wade contacted the National Institute of Allergy and Infectious Diseases NIAID about this funding [and it responded](#), "At no time did NIAID fund gain-of-function research to be conducted at WIV." As to the question of whether the Chinese lab did perform such research, NIAID says: "It is impossible for us to be aware of nor can we account for all of their activities." The money was laundered through Daszak but originally came from NIAID.

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6466186/>

ProGoFer's and Anti-GoFers

Microbiologists were divided into two camps ProGoFer's and Anti-GoFers. Fauci was a big proGoFer. In fact, when a controversy arose over making Avian Flu transmittable to humans Fauci wrote an [editorial](#) in WAPO defending it. If Fauci hadn't been a supporter of GoF / GoT and cracked down on Daszak, reported him to the FBI, instead of looking the other way, none of this would have happened. Fauci could have cut off the subaward grant money going to the WIV for years [INTERCEPT DOC page 91 et.al.](#) in a heartbeat. Not doing so, as a USG employees, Fauci, and his Deputy, Erik Stemmy, who signed off on the grants, were liable for violating the Executive Order banning GoF. Not only will either of these men face any criminal charges for their actions, but will remain in their NIH positions.

CHAPTER 18

THE CRITICS OF GoF/GoT PREDICTED IT WOULD CAUSE A PANDEMIC

"If one weighs the benefits verses risk of creating highly transmissible and highly fatal flu strains it should be clear that this research is better not done. If it is, then, at the very least, only labs with the highest level of safety protocols (P4) should be allowed to work with such strains, lesser safeguards are a breach of common sense. It is not an over reaction to think that a release of the most virulent strains might result in a pandemic which would be much worse than the pandemic of 1917, which killed more than 20 million people. Many strains being worked with today have a much higher fatality rate and could result in hundreds of millions, or billions of deaths." NYT comments: David Green Brooklyn NY June 30, 2014

DAVID RELMAN STANFORD UNIVERSITY MICROBIOLOGIST



SEPTEMBER 2014 David Relman: "My greatest fear is that someone will create a highly contagious and highly pathogenic infectious agent that does not currently exist in nature, publish its genetic blueprint, allow it to escape the laboratory by accident, or else enable a malevolent person or persons to synthesize the agent with the intention of releasing it in a deliberate manner. Although these may be unlikely scenarios, they could have catastrophic consequences, which is why I and others feel that we need to sensitize everyone to these possibilities and decide how to manage these risks ahead of time. I want to be clear: I am not opposed to laboratory work on dangerous pathogens, especially if they are known to exist in nature. Rather, I am opposed to high-risk experiments and, in particular, those that seek to create novel, dangerous pathogens that cannot be justified by well-founded expectations of near-term, critical benefits for public health — benefits that clearly outweigh the risks, and benefits that cannot be achieved through other means."

<https://med.stanford.edu/news/all-news/2014/09/5-questions--david-reلمان-on-risks-of-creating-new-pathogens.html>

MICROBIOLOGIST JONATHAN LATHAM



Dr. Latham: "Not only are there clear reasons to doubt that the wet market was the source, but it also requires you to accept the most staggering coincidence. After all, given that wet markets are widespread in China — indeed across much of Asia, how remarkable is it that the virus's zoonotic leap from animal to human just happened to take place in one that has a lab under 300 meters away, and another within 10 kilometres, that is researching not just bat coronaviruses, but the most closely related ones to the outbreak?" If you believe this is co-incidence you just fell off a turnip truck. Latham believes that SARS-CoV-19 close relative RaTG13 mutated in the miner's lungs in which it was discovered, was brought to the WIV and escaped.

<https://www.independentsciencenews.org/commentaries/a-proposed-origin-for-sars-cov-2-and-the-covid-19-pandemic/> GO BACK

DR. RICHARD EBRIGHT



Richard H. Ebright · Sep 7, 2021

@R_H_Ebright · Follow

Replying to @R_H_Ebright

The materials further reveal that the the grants also supported the construction--in Wuhan--of novel chimeric MERS-related coronaviruses that combined spike genes from one MERS-related coronavirus with genetic information from another MERS-related coronavirus.



Richard H. Ebright ·

@R_H_Ebright · Follow

The documents make it clear that assertions by the NIH Director, Francis Collins, and the NIAID Director, Anthony Fauci, that the NIH did not support gain-of-function research or potential pandemic pathogen enhancement at WIV are untruthful.

10:33 AM · Sep 7, 2021



18K



See the latest COVID-19 information on Twitter

[Read 798 replies](#)



Richard H. Ebright · Sep 7, 2021

@R_H_Ebright · Follow

Replying to @R_H_Ebright

...and thus not only was reasonably anticipated to exhibit enhanced pathogenicity, but, indeed, was *demonstrated* to exhibit enhanced pathogenicity.



Richard H. Ebright ·

@R_H_Ebright · Follow

The materials further reveal that the the grants also supported the construction--in Wuhan--of novel chimeric MERS-related coronaviruses that combined spike genes from one MERS-related coronavirus with genetic information from another MERS-related coronavirus.

10:33 AM · Sep 7, 2021



5.1K



See the latest COVID-19 information on Twitter

[Read 55 replies](#)

DR. RICHARD EBRIGHT OPPOSES BARIC'S GoF EXPERIMENTS AT UNIVERSITY OF NORTH CAROLINA AND WIV



Richard Ebright, a molecular biologist and biodefence expert at Rutgers University in Piscataway, New Jersey, told the *Daily Mail* that the odds of this new virus containing such unusual features and occurring naturally were 'possible – but improbable.' Ebright said scientists at the Wuhan Institute of Virology were creating chimeric coronaviruses (new hybrid micro-organisms) and seeking funding to test their ability to infect human cells while using procedures that leave no sign of human manipulation. Asked about the chance of a leak, he replied: "There definitely is a possibility. But there is no basis to say a high probability. It is clear that the Wuhan Institute of Virology was systematically constructing novel chimeric coronaviruses and was assessing their ability to infect human cells and human-**ACE2**-expressing mice."

"Other experiments in the University of North Carolina study show that the virus in wild bats would need to evolve to pose any threat to humans — a change that may never happen, although it cannot be ruled out. Baric and his team reconstructed the wild virus from its genome sequence and found that it grew poorly in human cell cultures and caused no significant disease in mice. "The only impact of this work is the creation, in a lab, of a new, non-natural risk," agrees Richard Ebright. Both Ebright and Wain-Hobson are long-standing critics of gain-of-function research. In their paper, the study authors also concede that funders may think twice about allowing such experiments in the future. "Scientific review panels may deem similar studies building chimeric viruses based on circulating strains too risky to pursue," they write, adding that discussion is needed as to "whether these types of chimeric virus studies warrant further investigation versus the inherent risks involved."



Simon Wain-Hobson, a virologist at the Pasteur Institute in Paris, points out that the researchers have created a novel virus that "grows remarkably well" in human cells. **"If the virus escaped, nobody could predict the trajectory,"** he says. Wain-Hobson disapproves of the study because, he says, it provides little benefit, and reveals little about the risk that the wild **SHC014** virus in bats poses to humans. Other scientists at the Pasteur Institute are part of the cover-up because they built the WIV. "Coronavirus outbreak in France not comes directly from China or Italy, say French scientists A genetic study conducted by scientists from France's Pasteur Institute suggests that the spread of the coronavirus epidemic in France is very little linked to cases imported from China."

http://www.xinhuanet.com/english/2020-04/30/c_139018917.htm

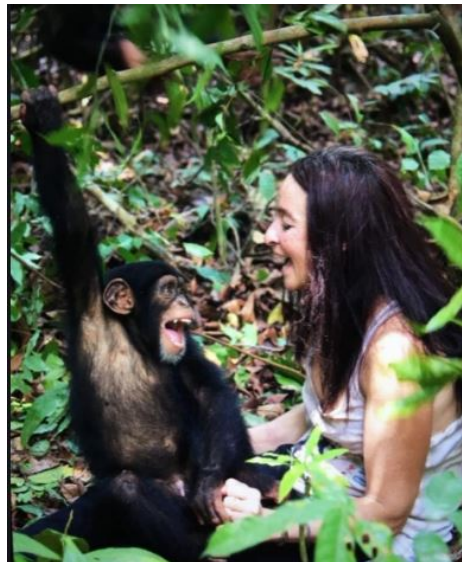
ALSO SEE: <https://www.nature.com/news/engineered-bat-virus-stirs-debate-over-risky-research>

<https://peterdaszak.com/wade.htm>

<https://www.nature.com/articles/nm.3985>

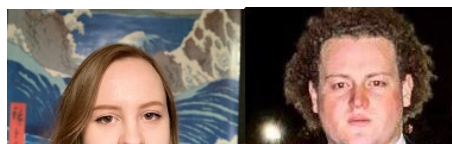
CHAPTER 19

DR. DASZAK'S BOGUS CREDENTIALS AND FAMILY BACKGROUND: "PETER COTTINGTON DASZAK" IS NOT HIS REAL NAME



JANET D COTTINGHAM

England & Wales, Civil Registration Marriage Index, 1916-2005 Peter Daszak Spouse JANET D COTTINGHAM <https://twitter.com/janetcottingha1> (Married Feb 1997) Is this a co-incidence or is Daszak hiding his Ukrainian background? Daszak's daughter interned at Eco-Health Alliance.





Kaspar Sebastian Bohdan Daszak is 20 years old and lives in an apartment in Stockholm. He lives with his mother Jacqueline Miura Daszak and John Ramstedt whose grandfather Gustaf John Ramstedt was a Finnish Charge D'Affairs to Japan.. BORN 8/27/2000. John's son. His home is valued at \$1,627,859.80 United States Dollars
<https://www.hitta.se/kaspar+daszak/stockholm/person/VgPwmnooOK>

CV: Peter Daszak holds a B.Sc. in Zoology in 1987 at University College of North Wales (UCNW), AKA Bangor University. Bangor is ranked #601-650 in QS Global World Rankings 2021 and 61st in the United Kingdom. Bio sketch Intercept docs "Bangor University (UK) BSc. (hons) 07/86 Zoology"

CV: Daszak earned a Ph.D. in parasitic infectious diseases in 1994 at University of East London. One would think he would return to graduate school to attain a degree in microbiology or infectious diseases but he lacks the mental capacity. Bio sketch Intercept docs: University of East London (UK) Ph.D 03/93 Infectious Diseases

University of East London



Key Information			
Rank 129	Location London, England	Established 1992	International Students 7%
Famous Courses Psychology, Architecture, Media		International Fees £11,880	

DASZAK INTERVIEW DECEMBER 2019



PETER DASZAK TALKS ABOUT HIS EARLY YEARS

Q. How did you become involved in zoology?

A. I was always interested in nature as a kid so I wanted to do zoology ever since I was eight years old I wanted to be a zoologist and I was on that truck. I did a zoology degree. I was going to work. I'm a reptile fan. I wanted to work on reptiles and then in England you have in your third year, you have to pick a research project, and I was late to the table and the only one left on reptiles was no good behavior stuff. It was ultra structure of a parasite in a lizard's gallbladder. I'll do it anyway but it was it was so fascinating I just got hooked on research. *I got hooked on seeing something for the first time and getting a result that tells you something that no one else has seen it.* I found that fascinating. I got a PhD in a similar field. I got a PhD in coccidiosis now that was the parasite. I did it in England, in London, near University of East London.

Q. Okay and did you do a postdoc after that?

A. Yeah I did a couple of postdocs. It was in a pretty bad time in England. There were one year postdocs and kept getting refunded but it's not great support.

Q. What areas were they in?

A. Similar stuff parasitology. I was a sort of general because I could do what from across country. I volunteered at CDC and it was during the Nipah virus outbreak and I was in the lab doing electronic respond the first samples.





CHAPTER 20

THE GRANTS THAT WERE APPROVED BY STEMMY AND FAUCI

Subject: Confidential -A new bat-origin coronavirus emerging in pigs in China discovered under our NIAID ROI Importance: High

Dear Dr Fauci and NIAID colleagues,

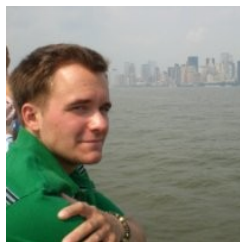
It was a pleasure to meet you again today. I've attached an unpublished paper, currently in the second round of review with Nature that describes a novel bat-origin Coronavirus (SADS-CoV: Swine Acute Diarrheal Syndrome coronavirus) that recently spilled over into pig farms in Southern China, leading to the death of over 25,000 piglets in 5+ farms in Guangdong Province. The virus originates in the same group of bats as SARS-CoV, and emerged in the same place. It's not known to be zoonotic (we've tested 35+ pig farm workers with an antibody assay and none are positive. The pig farm owners tell us the virus is now under control, thanks to culling and separation of infected herds. It's not yet known if this virus has appeared elsewhere, but we are looking. We're also doing assays to find out if it can infect human cells in the lab- so far no evidence of this. I hope this paper is of interest. You should know that this work was supported by a NIAID ROI that Erik Stemmy is the Program Officer for, and that I'm PI on, with Zhengli Shi as co-PI. If you want any other information at all, please don't hesitate to email or call and I'd be happy to come over to NIAID to brief you further. I'll also let you know if/when it will be published so that we can try to foster some publicity as appropriate. Cheers, Peter

[Judicial Watch](#)

OTHERS AT NIH WHO APPROVED DASZAK'S GRANTS

Laura A. Pone Grants Management Officer NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES

Grants Management Specialist: Jenny L. Greer



Grants Management Specialist: Adam Graham Phone: Fax: 301-493-0597 Assistant Grants Policy Officer at National Institutes of Health, Office of Extramural Research Dates Employed Mar 2016 – Jan 2019 Employment Duration 2 yrs 11 mos

- Evaluate management aspects of grant applications, including development of criteria and standards for planning, implementation, and evaluation of grant proposals.
- Monitor and execute all phases of awards of numerous mechanisms, including multi-project Cooperative Agreements, Small Business Innovative Research, Small Business Technology Transfer, Career Development Awards, Fellowships, Conference, and Training Program Grants.
- Provide guidance on statutes, regulations, policies, and procedures relevant to the award program in general and individual applications and proposals.
- Communications liaison for scientific program officers, institutional business officials, and principal investigators.

• Grants Management Coordinator for:

- o Global Infectious Disease Research Administrations Development Awards
- o Bi-Lateral Research Programs - China, India, Brazil, Indonesia
- o Vaccine Action Program (VAP) Small Research Grant Program (R03)
- o Systems Biology: The Next Generation for Infectious Diseases (Cooperative Agreements)

American University Degree Master of Arts (M.A.) Field Of Study International Economic Relations Dates attended or expected graduation 2007 – 2010 Specialization in the East Asia Region Significant Research Paper - Systemic Risk and Financial Regulation Recipient of the School of International Service Study Abroad Scholarship for study abroad in Malaysia University of Florida Degree Bachelor of Arts (B.A.) Field Of Study Political Science & Philosophy Dates attended or expected graduation 2001 – 2005

Grants Management Specialist: Shaun W Gratton Mount Airy, MD Age: 29 years old (301) 831-0856 kgratton@aol.com

CHAPTER 21

FORENSIC EVIDENCE OF LABORATORY MODIFICATION

Although Baric's "no-see-um" method was used to create SARS-CoV-19 making it almost impossible to determine the virus was unnatural Shi left some fingerprints:

THE AUSTRALIAN STUDY: SPIKE PROTEIN OPTIMIZED TO BIND TO HUMAN ACE2. IN SILICO COMPARISON OF SPIKE PROTEIN-ACE2 BINDING AFFINITIES ACROSS SPECIES; SIGNIFICANCE FOR THE POSSIBLE ORIGIN OF THE SARS-COV-2 VIRUS

- Sakshi Piplani^{1,2},
- Puneet Kumar Singh²
- David A. Winkler³⁻⁶
- Nikolai Petrovsky^{1,2*}

- 1 College of Medicine and Public Health, Flinders University, Bedford Park 5046, Australia
- 2 Vaxine Pty Ltd, 11 Walkley Avenue, Warradale 5046, Australia
- 3 La Trobe University, Kingsbury Drive, Bundoora 3042, Australia
- 4 Monash Institute of Pharmaceutical Sciences, Monash University, Parkville 3052, Australia
- 5 School of Pharmacy, University of Nottingham, Nottingham NG7 2RD. UK
- 6 CSIRO Data61, Pullenvale 4069, Australia

THE BINDING ENERGY BETWEEN SARS-COV-2 SPIKE PROTEIN AND ACE2 WAS HIGHEST FOR HUMANS OUT OF ALL SPECIES TESTED



"Notably, this approach surprisingly revealed that the binding energy between SARS-CoV-2 **Spike Protein** and **ACE2** was highest for humans out of all species tested, suggesting that SARS-CoV-2 **Spike Protein** is uniquely evolved to bind and infect cells expressing human **ACE2**. This finding is particularly surprising as, typically, a virus would be expected to have highest affinity for the receptor in its original host species, e.g. bat, with a lower initial binding affinity for the receptor of any new host, e.g. humans. However, in this case, the affinity of SARS-CoV-2 is higher for humans than for the putative original host species, bats, or for any potential intermediary host species. Although bats carry many coronaviruses including SARS-CoV, a relative of SARS-CoV-2, direct evidence for existence of SARS-CoV-2 in bats has not been found. As highlighted by our data, the binding strength of SARS-CoV-2 for bat **ACE2** is considerably lower than for human **ACE2**, suggesting that even if SARS-CoV-2 did originally arise from a bat precursor it must later have adapted its **Spike Protein** to optimise its binding to human **ACE2**. There is no current explanation for how, when or where this might have happened. Instances of direct human infection by coronaviruses or other bat viruses is rare with transmission typically involving an intermediate host. For example, lyssaviruses such as Hendra are periodically transmitted from bats to horses and then to humans who contact the infected horse. Similarly, SARS-CoV was shown to be transmitted from bats to civet cats and from them to humans. **To date, a virus identical to SARS-CoV-2 has not been identified in bats or any other non-human species, making its origins unclear.** To date, the most closely related coronavirus to SARS-CoV-2, is the bat coronavirus, BatCoV RaTG1, which has 96% whole-genome identity to SARS-CoV-2. 50. The fact that SARS-CoV-2 has also not been found in any likely intermediate host raises questions of the origins of the original SARS-CoV-2."

<https://arxiv.org/ftp/arxiv/papers/2005/2005.06199.pdf>

THE FORENSIC EVIDENCE OF LAB CREATION GAIN-OF-THREAT INSERTIONS AT POLYBASIC FURIN CLEAVAGE SITE PRRA IS EVIDENCE VIRUS WAS MODIFIED FOR INCREASED INFECTIVITY AND PATHOGENICITY - DR. RONEN SHEMESH

	S1/S2	S2'
Human SARS-CoV BJ01	655 - GICASYHTVSL----RSTS - 670	790 - DPLKPTKRSFIED - 802
Human SARS-CoV CUHK-W1	655 - GICASYHTVSL----RSTS - 670	790 - DPLKPTKRSFIED - 802
Human SARS-CoV Tor2	655 - GICASYHTVSL----RSTS - 670	790 - DPLKPTKRSFIED - 802
Human SARS-CoV Frankfurt-1	655 - GICASYHTVSL----RSTS - 670	790 - DPLKPTKRSFIED - 802
Human SARS-CoV Urbani	655 - GICASYHTVSL----RSTS - 670	790 - DPLKPTKRSFIED - 802
Civet SARS-CoV civet020	655 - GICASYHTVSL----RSTS - 670	790 - DPLKPTKRSFIED - 802
Civet SARS-CoV SZ16	655 - GICASYHTVSL----RSTS - 670	790 - DPLKPTKRSFIED - 802
Raccoon dog SARS-CoV A030	655 - GICASYHTVSL----RSTS - 670	790 - DPLKPTKRSFIED - 802
SARS-CoV-2	669 - GICASYQTQNSPRRA--SV - 688	808 - DPSKPSKRSFIED - 820
Pangolin CoV MP789	n/a - GICASYQTQNS----RSVS - n/a	n/a - DPSKPSKRSFIED - n/a
Bat SARS-CoV RaTG13	669 - GICASYQTQNS----RSVA - 684	804 - DPSKPSKRSFIED - 816
Bat SARS-CoV LYRa11	659 - GICASYHTASLL----RNTD - 674	794 - DPSKPTKRSFIED - 806
Bat SARS-CoV LYRa3	659 - GICASYHTASLL----RNTG - 674	794 - DPSKPTKRSFIED - 806
Bat SARS-CoV RaSHC014	656 - GICASYHTVSSL----RSTS - 671	791 - DPLKPTKRSFIED - 803
Bat SARS-CoV Rs4084	656 - GICASYHTVSSL----RSTS - 671	791 - DPLKPTKRSFIED - 803
Bat SARS-CoV WIV1	656 - GICASYHTVSSL----RSTS - 671	791 - DPLKPTKRSFIED - 803
Bat SARS-CoV Rs3367	656 - GICASYHTVSSL----RSTS - 671	791 - DPLKPTKRSFIED - 803
Bat SARS-CoV Rs7327	656 - GICASYHTVSSL----RSTS - 671	791 - DPLKPTKRSFIED - 803
Bat SARS-CoV Rs9401	656 - GICASYHTVSSL----RSTS - 671	791 - DPLKPTKRSFIED - 803
Bat SARS-CoV Rs4231	655 - GICASYHTVSSL----RSTS - 670	790 - DPLKPTKRSFIED - 802
Bat SARS-CoV WIV16	655 - GICASYHTVSSL----RSTS - 670	790 - DPLKPTKRSFIED - 802
Bat SARS-CoV Rs4874	655 - GICASYHTVSSL----RSTS - 670	790 - DPLKPTKRSFIED - 802
Bat SARS-CoV ZC45	646 - GICASYHTASIL----RSTS - 661	781 - DPSKPSKRSFIED - 793
Bat SARS-CoV ZXC21	645 - GICASYHTASIL----RSTG - 660	780 - DPSKPSKRSFIED - 792
Bat SARS-CoV Rf4092	634 - GICASYHTASLL----RGV - 649	769 - DPSKPTKRSFIED - 781
Bat SARS-CoV Rf/JL2012	636 - GICASYHTASLL----RSTG - 651	771 - DPLKPTKRSFIED - 783
Bat SARS-CoV JTM15	636 - GICASYHTASLL----RSTG - 651	771 - DPLKPTKRSFIED - 783
Bat SARS-CoV 16B0133	636 - GICASYHTASLL----RSTG - 651	771 - DPLKPTKRSFIED - 783
Bat SARS-CoV B15-21	636 - GICASYHTASLL----RSTG - 651	771 - DPLKPTKRSFIED - 783
Bat SARS-CoV YN2013	633 - GICASYHTASLL----RSIG - 648	768 - DPSKPTKRSFIED - 780
Bat SARS-CoV Anlong-103	633 - GICASYHTASLL----RSVG - 648	768 - DPSKPTKRSFIED - 780
Bat SARS-CoV Rf/Shaanxi2011	640 - GICASYHTASVL----RSTG - 655	775 - DPSKPTKRSFIED - 787
Bat SARS-CoV Rf/HuB2013	641 - GICASYHTASVL----RSTG - 656	776 - DPSKPTKRSFIED - 788
Bat SARS-CoV YNLF/34C	641 - GICASYHTASVL----RSTG - 656	776 - DPLKPTKRSFIED - 788
Bat SARS-CoV YNLF/31C	641 - GICASYHTASVL----RSTG - 656	776 - DPLKPTKRSFIED - 788
Bat SARS-CoV Rf1	641 - GICASYHTASHL----RSTG - 656	776 - DPLKPTKRSFIED - 788
Bat SARS-CoV Rf23	641 - GICASYHTASHL----RSTG - 656	776 - DPLKPTKRSFIED - 788
Bat SARS-CoV Rf/SX2013	639 - GICASYHTASLL----RSTG - 654	774 - DPLKPTKRSFIED - 786
Bat SARS-CoV Rf/HeB2013	641 - GICASYHTASLL----RSTG - 656	776 - DPLKPTKRSFIED - 788
Bat SARS-CoV Cp/Yunnan2011	641 - GICASYHTASLL----RNTG - 656	776 - DPSKPTKRSFIED - 788
Bat SARS-CoV Rs672	641 - GICASYHTASLL----RSVG - 656	776 - DPSKPTKRSFIED - 788
Bat SARS-CoV Rs4255	641 - GICASYHTASLL----RSVG - 656	776 - DPSKPTKRSFIED - 788
Bat SARS-CoV Rs4081	641 - GICASYHTASLL----RSVG - 656	776 - DPSKPTKRSFIED - 788
Bat SARS-CoV Rm1	641 - GICASYHTASVL----RSTG - 656	776 - DPSKPTKRSFIED - 788
Bat SARS-CoV Rf279	641 - GICASYHTASVL----RSTG - 656	776 - DPSKPTKRSFIED - 788
Bat SARS-CoV Rf/GX2013	642 - GICASYHTASVL----RSTG - 657	777 - DPSKPTKRSFIED - 789
Bat SARS-CoV Rs806	641 - GICASYHTASLL----RSTG - 656	776 - DPSKPTKRSFIED - 788
Bat SARS-CoV HKU3-1	642 - GICASYHTASVL----RSTG - 657	777 - DPSKPTKRSFIED - 789
Bat SARS-CoV Longquan-140	642 - GICASYHTASVL----RSTG - 657	777 - DPSKPTKRSFIED - 789
Bat SARS-CoV Rf3	641 - GICASYHTASLL----RSVG - 656	776 - DPSKPTKRSFIED - 788
Bat SARS-CoV Rs4247	642 - GICASYHTASLL----RSVG - 657	777 - DPSKPTKRSFIED - 789
Bat SARS-CoV Rs4237	641 - GICASYHTASLL----RSVG - 656	776 - DPSKPTKRSFIED - 788
Bat SARS-CoV As6526	641 - GICASYHTASLL----RSVG - 656	777 - DPSKPTKRSFIED - 789



No clear evolutionary pathway has been identified that would explain the presence of SARS-CoV-2's furin polybasic cleavage site, especially given its enhanced pathogenic significance. It is, therefore, not an unreasonable alternative to assume that the unique furin polybasic cleavage site found in SARS-CoV-2 and in no other close relatives may be the result of genetic manipulation. SARS-CoV-2 has a Furin Polybasic Cleavage Site PRRA that is not found in either bat, and pangolin viruses that were genetically similar to SARS-CoV-2. **This insertion interface makes it easy for the virus to infect humans because the spike protein on the virus immediately interacts with furin at the polybasic cleavage site.** Furin is an enzyme found abundantly in the body. Furin assists the virus envelope in merging with the cell membrane to infect it. Similar furin-like sites were also found in other viruses such as HIV and Ebola causing scientists to explore their similarities to SARS-CoV-2. This insertion allows the virus to skip animal to human transmission infect humans. SARS-CoV-2 has not been found in nature as SARS CoV-1

was. One can say it hasn't yet been found in nature but since the Corona Plague scientists have been looking desperately for this missing link. The coronaviruses causing SARS CoV-1 were descended from coronaviruses affecting masked civets and camels. Their genetic similarity was found to be 99 percent. This level of similarity was not found between bat and pangolin viruses or any other living creature, and SARS-CoV-2, because this is a creation of SHI ZHENG LI. Some scientists claim that inserting a new gene in a virus is like substituting a red brick for a black brick in a structure, but new insertion techniques, like passaging, leave no trace of human intervention.

THE INTELLIGENCE COMMUNITY WEIGHS IN

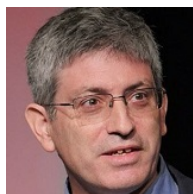
The IC assesses that public claims that some distinguishing features in SARS-CoV-2 are the result of genetic engineering are not diagnostic of genetic engineering. The IC has been evaluating how SARS-CoV-2 could have developed these features and notes that the furin cleavage site (FCS)—a region in the spike protein that enables infection and has been the topic of open-source debate—can also be consistent with a natural origin of the virus. We do not fully understand the diversity of natural coronaviruses or how often they recombine, suggesting that there are plausible natural means by which these features in SARS-CoV-2 could have emerged beyond what we currently understand.

- For example, the author of an article in April notes the SARS-CoV-2's FCS is unique among known betacoronaviruses. The author argues that such features are rare and so well-adapted for human infection that they are more likely emerged from laboratory work than from natural selection.

- Although an IC review of scientific literature has indicated that no known betacoronaviruses in the same subgenus have this FCS in the same region of the spike protein as SARS-CoV-2, similar FCSs are present in the same region of the spike protein as other naturally occurring coronaviruses, according to scientific articles.

CARL ZIMMER PUSHES "CAME FROM NATURE" THEORY: NEWLY DISCOVERED BAT VIRUSES GIVE HINTS TO COVID'S ORIGINS

Coronaviruses discovered in Laotian bats are surprisingly adept at infecting human cells, showing that such deadly features can indeed evolve outside of a lab. Three of the Laos coronaviruses were unusual: They carried a molecular hook on their surface that was very similar to the hook on the virus that causes Covid-19, called SARS-CoV-2. Like SARS-CoV-2, their hook allowed them to latch onto human cells. "That really puts to bed any notion that this virus had to have been concocted, or somehow manipulated in a lab, to be so good at infecting humans," said Michael Worobey, a University of Arizona virologist who was not involved in the work.



With the novel viruses here described, the pool of sequences found in *Rhinolopus* spp. allows the reconstitution of a genome sufficiently close to that of SARS-CoV-2 without the need to hypothesize recombination or natural selection for increased RBD affinity for hACE2 in an intermediate host before spillover³⁸, nor natural selection in humans following spillover³⁹. **However, we found no furin site in any of these viruses on sequences determined from original fecal swab samples, devoid of any bias associated with counterselection of the furin site by amplification in Vero cells.** Lack of furin cleavage may be explained by insufficient sampling in bats, or by acquisition of the furin cleavage site through passages of the virus in an alternate host or during an early poorly symptomatic unreported circulation in humans. Finally, where these intergenomic recombinations arose and the epidemiological link with the first human cases remains to be established...Despite the absence of the furin site in these novel bat sarbecoviruses, phylogenetic reconstruction of this fragment, key for the virus tropism and host spectrum, revealed that Laotian *R. malayanus* BANAL-52, *R. pusillus* BANAL-103, and *R. marshalli* BANAL-236 coronaviruses are the closest ancestors of SARS-CoV-2 known to date. **Identification of strains of animal origin with a furin cleavage site may require additional sampling...**To conclude, our results pinpoint the presence of new bat sarbecoviruses that **seem to have the same potential for infecting humans as early strains of SARS-CoV-2.** People working in caves, such as guano collectors, or certain ascetic religious communities who spend time in or very close to caves, as well as tourists who visit the caves, are particularly at risk of being exposed. Further investigations are needed to assess if such exposed populations have been infected by one of these viruses, if these infections are associated with symptoms, and whether they could confer protection against subsequent SARS-CoV-2 infections. [Zimmer NYT](#)

THE NEW YORK TIMES AND CARL ZIMMER GIVES MICHAEL WOROBEY THEORY FRONT PAGE STATUS

Zimmer took over the science beat after Donald MacNeil was fired for using the word nigger in a lecture on racist language. While he was still at the Times Donald wrote "I was offended by Nicholas Wade's attacks on Dr. Anthony S. Fauci of the National Institutes of Health and Peter Daszak of the EcoHealth Alliance, both of whom I have known for years; I know both are dedicated to saving lives, and they have always told me the truth — or what they honestly believed to be the truth at the time, because evidence sometimes changes. They are now both getting death threats, and that is repulsive."

Zimmer earned his BA from Yale University. He wrote for Discover Magazine and later gained attention in 2013 when he started writing his column Matter in The New York Times. Also see [NYT Zimmer often uses Kristian Anderson as a source.](#)

ALEKSEI CHMURA: SHADY ECO-CON MAN ECOHEALTH ALLIANCE VICE PRESIDENT WHO WORKS WITH DASZAK ORCHESTRATES ARTICLE TO SHOW FURIN

A NOVEL POTENTIALLY RECOMBINANT RODENT CORONAVIRUS WITH A POLYBASIC CLEAVAGE SITE IN THE SPIKE PROTEIN August 25, 2021

Authors: Xin Li, Liang Wang, Peipei Liu, Hongying Li, Shuting Huo, Kexin Zong, Shiyan Zhu, , Yuanyuan Guo, Libiao Zhang, Ben Hu, Yu Lan, ALEKSEI CHMURA <https://orcid.org/0000-0001-5544-0431>, Guizhen Wu, **Peter Daszak**, William J. Liu and target="_blank">George F. Gao : <https://doi.org/10.1128/JVI.01173-21> • Check for updates on crossmark Preprint 5 August 2021

ABSTRACT

"The emergence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has reignited global interest in animal coronaviruses and their potential for human transmission. While bats are thought to be the wildlife reservoir of SARS-CoV and SARS-CoV-2, the widespread human coronavirus OC43 is thought to have originated in rodents. We sampled 297 rodents and shrews representing eight species in three municipalities of southern China. We report coronavirus prevalence of 23.3% and 0.7% in Guangzhou and Guilin, respectively, with samples from urban areas having significantly

higher coronavirus prevalence than those from rural areas. We obtained three coronavirus genome sequences from *Rattus norvegicus*, including a Betacoronavirus RCoV-GCCDC3, an Alphacoronavirus RCoV-GCCDC5 and a novel Betacoronavirus RCoV-GCCDC4. Recombination analysis suggests that there was a potential recombinant event involving RCoV-GCCDC4, Murine hepatitis virus and Longquan RI rat coronavirus. **Furthermore, we uncovered a polybasic cleavage site RARR in the spike (S) protein of RCoV-GCCDC4, which is dominant in RCoV.** These findings provide further information on the potential for inter-species transmission of coronaviruses and demonstrate the value of a One Health approach to virus discovery. Importance: surveillance of viruses among rodents within rural and urban areas of South China identified three rodent coronaviruses RCoV-GCCDC3, 4 and 5, one of which was identified as a novel potentially recombinant coronavirus with a polybasic cleavage site in the spike (S) protein. Through reverse transcription PCR screening of coronaviruses, we found that coronavirus prevalence in urban areas is much higher than that in rural areas. Subsequently, we obtained three coronavirus genome sequences by deep sequencing. After different method-based analyses, we found that RCoV-GCCDC4 was a novel potentially recombinant coronavirus with a polybasic cleavage site in S protein, dominant in RCoV. This newly identified coronavirus RCoV-GCCDC4 with its potentially recombinant genome and polybasic cleavage site provides a new insight into the evolution of coronaviruses. Furthermore, our results provide further information on the potential for inter-species transmission of coronaviruses and demonstrate the necessity of a One Health approach for zoonotic disease surveillance.

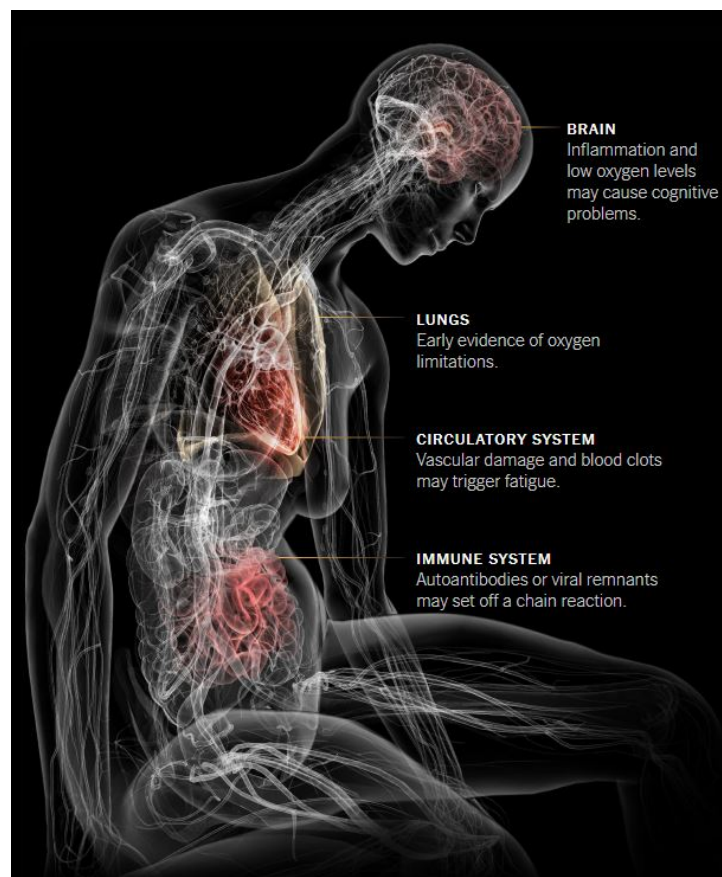
ARGININE / FURIN



1. Originally identified in 1990, furin is a cellular endoprotease that proteolytically activates many proprotein substrates ranging from pathogenic agents to growth factors, receptors, and extracellular matrix proteins. The furin cleavage site is a small region of SARS-CoV-2 **Spike Protein** just 12 units of its 30,000-unit genome. A virus usually acquires inserts like this by accidentally exchanging genomic units with another virus when both invade the same cell. **But no other known virus in SARS2's group has this 12-unit insert.** No one has yet found the human population in which the virus might have evolved this way. The insert also contains entities known as arginine codons, which are common in humans but not in coronaviruses like SARS2. "Since 1992 the virology community has known that the one sure way to make a virus deadlier is to give it a furin cleavage site," writes [Dr. Steven Quay](#), a biotech entrepreneur interested in the origins of SARS2. "At least 11 such experiments have been published, including one by Dr. Shi." David Baltimore, an eminent virologist and former president of the California Institute of Technology stated: "When I first saw the furin cleavage site in the viral sequence, with its [arginine](#) codons, I said to my wife it was the smoking gun for the origin of the virus. These features make a powerful challenge to the idea of a natural origin for SARS2," he said. Baltimore is currently President Emeritus and distinguished Professor of Biology at Caltech. Awarded the Nobel Prize at the age of 37 for research in virology, Baltimore has profoundly influenced national science policy on such issues as recombinant DNA research and the AIDS epidemic. After being pressured by the Fauci Mafia, Baltimore [walked some of this back](#).

CHAPTER 22

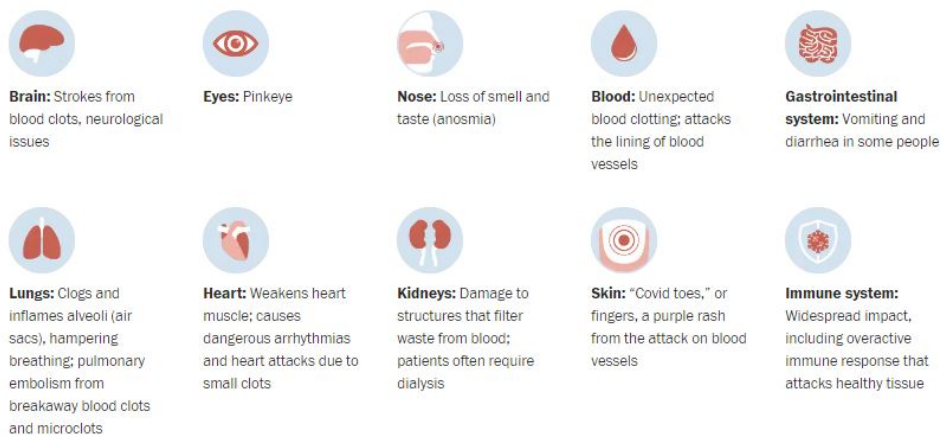
GAIN-OF-FUNCTION / GAIN-OF-THREAT MADE A COVID-19, THAT OCCURRED IN NATURE, MORE TRANSMITTABLE AND MORE LONG LASTING



One indication that this virus was made more deadly and communicable by the Chinese scientists encouraged by Daszak and Fauci is that it doesn't act like any other virus did. It is far more deadly and causes many other symptoms other than respiratory disease. It attacks children with a Kawasaki disease - an illness that causes inflammation (swelling and redness) in blood vessels throughout the body. It happens in three phases, and a lasting fever usually is the first sign. The condition most often affects kids younger than 5 years old. *National Geographic* reports on these weird symptoms but is afraid to even suggest they may be a result of Gain-of-

Purpose experiments. Lynne Turner-Stokes, professor of rehabilitation medicine at King's College, says Covid is a "multi-system disease" which can potentially affect any organ. It causes microvascular problems and clots. Lungs, brain, skin, kidneys and the nervous system may be affected. Neurological symptoms can be mild (headache) or severe (confusion, delirium, coma). Turner-Stokes says it's uncertain why the illness is sometimes so protracted. One explanation is that the body's immune system goes into overdrive, with an ongoing reaction. Another is that the symptoms are virus-driven. Either way, she says there can be a "recrudescence of symptomatology". Or, as she also puts it using more colloquial language, "the whole caboodle comes back." The most common post-Covid symptom is parosmia, loss of smell. [which scientists attribute to the ACE2 invasion](#). Paediatric inflammatory multisystem syndrome temporally associated with SARS-CoV-2 (PIMS-TS) is a new, rare, post-infectious complication of SARS-CoV-2 infection in children. In a study of veterans, Covid survivors were 35 percent more likely than other patients to have long-term kidney damage or declines in kidney function. Covid-19 may cause greater loss of gray matter and tissue damage in the brain than naturally occurs in people who have not been infected with the virus, a large new study found. The study, published in the journal *Nature*, is believed to be the first involving people who underwent brain scans both before they contracted Covid and months after. Covid patients in the study — who underwent their second brain scan an average of four and a half months after their infection — lost more than noninfected participants, experiencing between 0.2 percent and 2 percent additional gray matter loss in different brain regions over the three years between scans. They also lost more overall brain volume and showed more tissue damage in certain areas. [NATURE](#) The coronavirus may infect tissue within the male genital tract, new research on rhesus macaques shows. The finding suggests that symptoms like erectile dysfunction reported by some Covid patients may be caused directly by the virus, not by inflammation or fever that often accompany the disease. The research demonstrated that the coronavirus infected the prostate, penis, testicles and surrounding blood vessels in three male rhesus macaques. The monkeys were examined with whole body scans specially designed to detect sites of infection. [NYT](#)

Symptoms of covid-19 appear to include:



<https://www.nationalgeographic.com/science/2020/05/kawasaki-stroke-why-coronavirus-weirdest-symptoms-are-only-emerging-now-cvd>

<https://www.theguardian.com/world/2020/may/15/weird-hell-professor-advent-calendar-covid-19-symptoms-paul-garner>

Detailed Study of Post Covid Symptoms

"There is a bidirectional relationship between Covid-19 and diabetes. On the one hand, diabetes is associated with an increased risk of severe Covid-19. On the other hand, new-onset diabetes and severe metabolic complications of preexisting diabetes, including diabetic ketoacidosis and hyperosmolality for which exceptionally high doses of insulin are warranted, have been observed in patients with Covid-19. 1-3 These manifestations of diabetes pose challenges in clinical management and suggest a complex pathophysiology of Covid-19-related diabetes."

<https://www.nejm.org/doi/full/10.1056/NEJMc2018688>

In general, SARS begins with a high fever (temperature greater than 100.4°F [$>38.0^{\circ}\text{C}$]). Other symptoms may include headache, an overall feeling of discomfort, and body aches. Some people also have mild respiratory symptoms at the outset. About 10 percent to 20 percent of patients have diarrhea. After 2 to 7 days, SARS patients may develop a dry cough. Most patients develop pneumonia. <https://www.cdc.gov/sars/about/fs-sars.html> A study published in the *Journal of International Audiology* that looked at nearly 60 case reports and studies found that 15 percent of adults with Covid-19 reported symptoms of tinnitus. The study of 100 patients from 21 states, published in *The Annals of Clinical and Translational Neurology*, found that 85 percent of them experienced four or more neurological issues like brain fog, headaches, tingling, muscle pain and dizziness. A small number of Covid patients who had never experienced mental health problems are developing severe psychotic symptoms weeks after contracting the coronavirus. A condition, which the Centers for Disease Control and Prevention are calling Multisystem Inflammatory Syndrome in Children, has shaken widespread confidence that children were largely spared from the pandemic. Instead of targeting lungs as the primary coronavirus infection does, it causes inflammation throughout the body and can cripple the heart.

CHAPTER 23

CHRONOLOGY





DECEMBER 2006 DASZAK AND SHI ZHENG LI

1970s, Researchers were learning for the first time to move genes from one organism to another to make bacteria produce human insulin. From the start, critics worried that such experiments could accidentally create deadly pathogens if they escaped from labs.

HIGH RECOMBINATION AND MUTATION RATES IN MOUSE HEPATITIS VIRUS SUGGEST THAT CORONAVIRUSES MAY BE POTENTIALLY IMPORTANT EMERGING VIRUSES

1995 Abstract: Coronaviruses are common respiratory and gastrointestinal pathogens of mammals and birds. Not only do they cause about 15–20% of the common colds in humans, they are also occasionally associated with infections of the lower respiratory tract and central nervous system. The prototype, mouse hepatitis virus (MHV), contains a 32 kb genomic RNA which encodes two large orfs at the 5' end, designated orf 1a and orf 1b. Orf 1b contains highly conserved polymerase, helicase and metal binding motifs typical of viral RNA polymerases while orf 1a contains membrane and cysteine rich domains, and serine- and poliovirus 3c-like protease motifs¹. **The large size of the genome coupled with its unique replication strategy and high recombination frequencies during mixed infection predict a considerable capacity to evolve.** Ralph S. Baric Kaisong FuWan Chen / Boyd Yount University of North Carolina

https://link.springer.com/chapter/10.1007/978-1-4615-1899-0_91

REVERSE GENETICS WITH A FULL-LENGTH INFECTIOUS CDNA OF SEVERE ACUTE RESPIRATORY SYNDROME CORONAVIRUS

OCTOBER 2003 Baric published the results of his research: "A previously undescribed coronavirus (CoV) is the etiologic agent responsible for severe acute respiratory syndrome (SARS). Using a panel of contiguous cDNAs that span the entire genome, **we have assembled a full-length cDNA of the SARS-CoV Urbani strain¹** and have rescued molecularly cloned SARS viruses (**infectious clone SARS-CoV**) that contained the expected marker mutations inserted into the component clones. Recombinant viruses² replicated as efficiently as WT virus and both were inhibited by treatment with the cysteine proteinase inhibitor (2S,3S)-transepoxy succinyl-L-leucylamido-3-methylbutane ethyl ester. In addition, subgenomic transcripts were initiated from the consensus sequence ACGAAC in both the WT and infectious clone SARS-CoV. **Availability of a SARS-CoV full-length cDNA provides a template for manipulation of the viral genome, allowing for the rapid and rational development and testing of candidate vaccines and therapeutics against this important human pathogen.** Our cloning and assembly strategy generated an infectious clone within 2 months of identification of the causative agent of SARS, providing a critical tool to study coronavirus pathogenesis and replication. The availability of coronavirus infectious cDNAs heralds a new era in coronavirus genetics and genomic applications, especially within the replicase proteins whose functions in replication and pathogenesis are virtually unknown.

<https://pubmed.ncbi.nlm.nih.gov/14569023>

1. The Urbani strain was sequenced by the US Centers for Communicable Diseases in Atlanta, Georgia. It is a common strain in Asia, named after Carlo Urbani, who was an infectious disease specialist at the World Health Organization's office in the Vietnamese capital, Hanoi. He helped to identify the disease as a coronavirus but later died from it.

www.sciencemag.org/cgi/rapidpdf/1085952v1.pdf

2. Viral recombination occurs when viruses of two different parent strains coinfect the same host cell and interact during replication to generate virus progeny that have some genes from both parents.

2004 The Chinese and French governments signed a cooperation agreement on fighting and preventing new diseases, stressing the active cooperation between China and France in the construction of high-level biosafety laboratories and the system construction of biosafety laws and regulations etc. In order to implement the spirit of Sino-French agreement, in 2005, Wuhan Institute of Virology undertook the task of building a national biosafety laboratory of Wuhan, Chinese Academy of Sciences. With nearly 10 years of unremitting efforts, the laboratory completed the physical facilities in January 2015. In August 2016, it obtained the recognition and authentication certificate for the critical protection equipment installation and commissioning.

2002-2004 THE WIV SCIENTISTS BEGAN COLLECTING BAT VIRUS SINCE THE SARS-1 OUTBREAK

2004 according to *Scientific American*, a team from the WIV led by virologist **Shi Zhengli** began visiting caves in southern China, hoping to find the cause of SARS. They captured bats and took blood, saliva, and fecal samples, and tested the samples for viruses back in Wuhan.

DEVELOPMENT OF MOUSE HEPATITIS VIRUS MHV AND SARS-COV INFECTIOUS CDNA CONSTRUCTS (BARIC)

FEBRUARY 2005 ABSTRACT: The genomes of transmissible gastroenteritis virus (TGEV) and Mouse Hepatitis Virus (MHV) have been generated with a novel construction strategy that allows for the assembly of very large RNA and DNA genomes from a panel of contiguous cDNA subclones. Recombinant viruses generated from these methods contained the appropriate marker mutations and replicated as efficiently as wild-type virus. **The MHV cloning strategy can also be used to generate recombinant viruses that contain foreign genes or mutations at virtually any given nucleotide.** MHV molecular viruses were engineered to express green fluorescent protein (GFP), demonstrating the feasibility of the systematic assembly approach to create recombinant viruses expressing foreign genes. **The systematic assembly approach was used to develop an infectious clone of the newly identified human coronavirus, the severe acute respiratory syndrome virus (SARS-CoV).** Our cloning and assembly strategy

generated an infectious clone within 2 months of identification of the causative agent of SARS, providing a critical tool to study coronavirus pathogenesis and replication. The availability of coronavirus infectious cDNAs heralds a new era in coronavirus genetics and genomic applications, especially within the replicase proteins whose functions in replication and pathogenesis are virtually unknown.

https://www.researchgate.net/publication/8119695_Development_of_mouse_hepatitis_virus_and_SARS-CoV_infectious_cDNA_constructs

COMPOSITIONS OF CORONAVIRUSES WITH A RECOMBINATION-RESISTANT GENOME (BARIC)

JANUARY 19, 2006 "In further embodiments, the present invention provides a helper cell for producing an infectious, multiplication-defective, coronavirus particle, comprising: (a) a SARS coronavirus replicon RNA comprising a coronavirus packaging signal and a heterologous RNA sequence, wherein said replicon RNA lacks a sequence encoding at least one coronavirus structural protein; and/or (b) at least one separate helper RNA encoding the at least one coronavirus structural protein absent from the replicon RNA, said helper RNA lacking a coronavirus packaging signal; wherein the combined expression of the replicon RNA and the helper RNA produces an infectious, multiplication-defective coronavirus particle. Thus, the present invention includes the embodiment of a helper cell comprising a helper RNA encoding at least one coronavirus structural protein and the embodiment of a helper cell comprising a SARS coronavirus replicon RNA comprising a coronavirus packaging signal and a heterologous RNA sequence, wherein said replicon RNA lacks a sequence encoding at least one coronavirus structural protein.

The present invention additionally provides a method of making infectious, multiplication-defective, coronavirus particles, comprising: a) providing the helper cell of this invention; and b) producing coronavirus particles in the helper cell.... "Multiplication-defective" or "replication-defective" as used herein means that the replicon RNA contained within viral particles produced according to the present invention does not itself contain sufficient genetic information to allow for the production of new infectious viral particles.

<https://patents.justia.com/patent/7618802>

2006 Baric was granted a patent for his invisible method of fabricating a full-length infectious clone using the seamless, no-see'm method. But this time, it wasn't a clone of the mouse-hepatitis virus — it was a clone of the entire deadly human SARS virus, the one that had emerged from Chinese bats, via civets, in 2002. The Baric Lab came to be known by some scientists as "the Wild Wild West." Also in **2006** Baric hoping to come up with a "vaccine strategy" for SARS, produced noninfectious virus replicon particles (or VRPs) using the Venezuelan-equine-encephalitis virus¹ which they fitted with various SARS **Spike Proteins**. Then, wearing Tyvek suits and two pairs of gloves each, and working in a biological safety cabinet in a BSL-3-certified laboratory, they cloned and grew recombinant versions of the original SARS virus in an incubator in a medium that held African-green-monkey cells. When they had grown enough virus, the scientists swapped out one kind of **Spike Protein** for a carefully chosen mutant, and they challenged their prototype vaccine with it in mice. <https://nymag.com/intelligencer/article/coronavirus-lab-escape-theory.html>

1. VEEV was developed as a biological weapon by the United States and Soviet Union during the Cold War. It was manufactured as an incapacitating agent, designed to cause severe symptoms that would not only weaken the opposing military, but also require valuable resources to contain and treat.

2006 Shi and Daszak collaborated with a researcher in Australia to publish "Review of bats and SARS" in Emerging Infectious Diseases, a peer-reviewed journal published monthly by the U.S. Centers for Disease Control and Prevention. Shi was again listed as the second author, and the work was funded by the same PRC and NIH/NSF grants referenced above.

REVIEW OF BATS AND SARS

DECEMBER 2006 Shi Zheng Li a researcher at Wuhan Institute of Virology co-authors an article with Peter Daszak describing whole-genome sequences of two novel bat coronaviruses from Chinese horseshoe bats that target the **ACE2 - ANGIOTENSIN-CONVERTING ENZYME 2** receptor, just like SARS-CoV-2 does¹ Abstract: Bats have been identified as a natural reservoir for an increasing number of emerging zoonotic viruses, including henipaviruses and variants of rabies viruses. Recently, we and another group independently identified several horseshoe bat species (genus *Rhinolophus*) as the reservoir host for a large number of viruses that have a close genetic relationship with the coronavirus associated with severe acute respiratory syndrome (SARS). Our current research focused on the identification of the reservoir species for the progenitor virus of the SARS coronaviruses responsible for outbreaks during 2002–2003 and 2003–2004. In addition to SARS-like coronaviruses, **many other novel bat coronaviruses**, which belong to groups 1 and 2 of the 3 existing coronavirus groups, have been detected by PCR.² The discovery of bat SARS-like coronaviruses and the great genetic diversity of coronaviruses in bats have shed new light on the origin and transmission of SARS coronaviruses.

https://wwwnc.cdc.gov/eid/article/12/12/06-0401_article

1. In 2000, when a different coronavirus struck, Michael Farzan and his team figured out how it was getting into human cells: targeting a specific receptor called **ACE2** found on certain cells. A chimeric virus is a genetic chimerism or chimera is a single organism composed of cells with more than one distinct genotype. It is a virus that has not been found in nature.

2. Polymerase Chain Reaction (PCR) is a method to rapidly make millions to billions of copies (complete copies or partial copies) of a specific DNA sample, allowing scientists to take a very small sample of DNA and amplify it (or a part of it) to a large enough amount to study in detail. [A similar Shi Zheng Li and Daszak paper.](#)

2007 Baric said that we had entered "the Golden Age of Coronavirus Genetics." Baric is basically the inventor of GoT.

GIVING A SARS-LIKE VIRUS THE ABILITY TO INFECT HUMANS IS GAIN-OF-THREAT





Difference in Receptor Usage between Severe Acute Respiratory Syndrome (SARS) Coronavirus and SARS-Like Coronavirus of Bat Origin[▽]

Wuze Ren,^{1,†} Xiuxia Qu,^{2,†} Wendong Li,^{1,‡} Zhenggang Han,¹ Meng Yu,³ Peng Zhou,¹ Shu-Yi Zhang,⁴ Lin-Fa Wang,^{3,*} Hongkui Deng,² and Zhengli Shi^{1,*}

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State Key Laboratory of Virology, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China,¹ Key Laboratory of Cell Proliferation and Differentiation of the Ministry of Education, College of Life Sciences, Peking University, Beijing, China,² CSIRO Livestock Industries, Australian Animal Health Laboratory and Australian Biosecurity Cooperative Research Center for Emerging Infectious Diseases, Geelong, Australia,³ School of Life Science, East China Normal University, Shanghai, China⁴

*Corresponding author. Mailing address for Z. Shi: State key Laboratory of Virology, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, Hubei 430071, China. Phone: (86-27)-87197240. Fax: (86-27)-87197240.

E-mail: zishi@wh.iov.cn. Mailing address for L.-F. Wang: CSIRO Livestock Industries, Australian Animal Health Laboratory, P.O. Bag 24, Geelong, Victoria 3220, Australia. Phone: (61-3)-52275121. Fax: (61-3)-52275555.

E-mail: Linfa.wang@csiro.au

[†]W.R. and X.Q. contributed equally to this work.

[‡]Present address: School of Life Science, Heilongjiang University, Harbin, 150080, China.

2007 "A group of SARS-like CoVs (SL-CoVs) has been identified in horseshoe bats. SL-CoVs and SARS-CoVs share identical genome organizations and high sequence identities, with **the main exception of the N terminus of the Spike Protein (S)**, known to be responsible for receptor binding in CoVs. **In this study, we investigated the receptor usage of the SL-CoV S by combining a HIV human immunodeficiency virus-based pseudovirus system with cell lines expressing the ACE2 molecules of human, civet, or horseshoe bat.** In addition to full-length S of SL-CoV and SARS-CoV, a series of S chimeras was constructed by inserting different sequences of the SARS-CoV S into the SL-CoV S backbone. Several important observations were made from this study. First, the SL-CoV S was unable to use any of the three **ACE2** molecules as its receptor. Second, the SARS-CoV S failed to enter cells expressing the bat ACE2. **Third, the chimeric S covering the previously defined receptor-binding domain gained its ability to enter cells via human ACE2, albeit with different efficiencies for different constructs.** Fourth, a minimal insert region (amino acids 310 to 518) was found to be sufficient to convert the SL-CoV S from non-**ACE2** binding to human **ACE2** binding, indicating that the SL-CoV S is largely compatible with **SARS-CoV S PROTEIN** both in structure and in function. The significance of these findings in relation to virus origin, virus recombination, and host switching is discussed."

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2258702>



ANALYSIS: The three most important phrases in this abstract as they relate to SARS-CoV-2 are: "First, the SL-CoV S was unable to use any of the three **ACE2** molecules as its receptor." Second "We investigated the receptor usage of the SL-CoV S by combining a human immunodeficiency virus-based pseudovirus system with cell lines expressing the **ACE2** molecules of human, civet, or horseshoe bat" "Third, the chimeric S covering the previously defined receptor-binding domain gained its ability to enter cells via human **ACE2**."

In layman's terms: We found this SARS-like virus ("S") that couldn't infect human cells. So, we combined S with parts of HIV, which does infect human cells, to see if this new S could infect human cells. The new S ("chimeric S") can infect human cells. We find that WIV was involved in this study in the Materials and Methods section: "Materials and Methods A MAb against p24 of HIV was generated by the HIV group of the Wuhan Institute of Virology (unpublished results). Rabbit polyclonal antibodies against **ACE2** of the bat *R. pearsonii* (RpACE2) was generated using a recombinant RpACE2 protein expressed in *Escherichia coli* at our laboratory at the Wuhan Institute of Virology, following standard procedures. All 10 scientists who are associated with this paper are also associated with the **Wuhan Institute of Virology**."

SHI ZHENGLI: DIFFERENCE IN RECEPTOR USAGE BETWEEN SEVERE ACUTE RESPIRATORY SYNDROME (SARS) CORONAVIRUS AND SARS-LIKE CORONAVIRUS OF BAT ORIGIN

FEBRUARY 2008 In this study, a human immunodeficiency virus (HIV)-based pseudovirus system was employed to address these issues.¹ Our results indicated that the SL-CoV S protein is unable to use ACE2 proteins of different species for cell entry and that SARS-CoV S protein also failed to bind the ACE2 molecule of the horseshoe bat, *Rhinolophus pearsonii*. **However, when the RBD of SL-CoV S was replaced with that from the SARS-CoV S, the hybrid S PROTEIN was able to use the huACE2 [HumanACE2] for cell entry, implying that the SL-CoV S proteins are structurally and functionally very similar to the SARS-**

CoV S. These results suggest that although the SL-CoVs discovered in bats so far are unlikely to infect humans using ACE2 as a receptor, it remains to be seen whether they are able to use other surface molecules of certain human cell types to gain entry. **It is also conceivable that these viruses may become infectious to humans if they undergo N-terminal sequence variation, for example, through recombination with other CoVs, which in turn might lead to a productive interaction with ACE2 or other surface proteins on human cells.**

1. Whether it is possible to construct an ACE2-binding SL-CoV S protein by replacing the RBD with that from SARS-CoV S proteins is also unknown.

The significance of these findings is as follows. First, the failure of SARS-CoV S protein to use bat RpACE2 as a receptor suggests that despite the presence of a diverse group of SL-CoVs in horseshoe bats, they are unlikely to be the natural reservoir of the immediate progenitor virus for SARS-CoV. It is therefore important to continue the search for the reservoir of SARS-CoV in other bat and wildlife species. It is also important to conduct such searches in different geographical locations because live-animal markets in southern China source their animals from all over China and from foreign countries and it is possible that the natural host of SARS-CoV was not indigenous to the site of the first SARS outbreak. **Second, as predicted, sequence variation in the N-terminal region of the SL-CoV S protein rendered it incapable of using ACE2 as a receptor for cell entry. However, the ACE2-binding activity of SARS-LIKE-CoVs was easily acquired by the replacement of a relatively small sequence segment of the S protein from the SARS-CoV S sequence, highlighting the potential dangers posed by this diverse group of viruses in bats. It is now well documented that bat species, including horseshoe bats, can be infected by different CoVs. Coinfection by different CoVs in an individual bat has also been observed. Knowing the capability of different CoVs to recombine both in the laboratory and in nature, the possibility that SL-CoVs may gain the ability to infect human cells by acquiring S sequences competent for binding to ACE2 or other surface proteins of human cells can be readily envisaged.** This could occur if the same bat cells carry receptors for both types of viruses. In this context, it could be concluded that the particular horseshoe bat species investigated in the current study is unlikely to be the putative mixing host. However, one cannot rule out the possibility that a different horseshoe bat or a different bat species might have a functional ACE2, thus giving it the ability to act as a mixing host. This work was jointly funded by a State Key Program for Basic Research Grant (2005CB523004) from the Chinese Ministry of Science and Technology, a special fund from the president of the Chinese Academy of Sciences (no. 1009), the Knowledge Innovation Program Key Project of the Chinese Academy of Sciences.

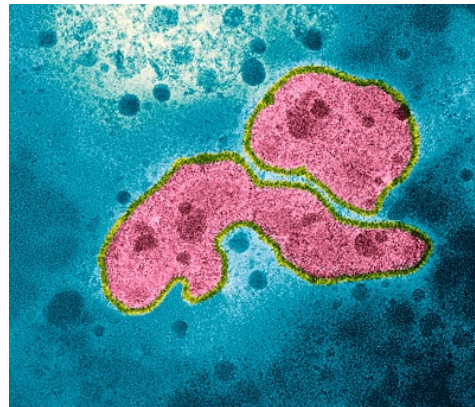
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2258702/>

PETER DASZAK: RISK OF VIRAL EMERGENCE FROM BATS (DASZAK)

SEPTEMBER 2008 Using a range of in vitro techniques (including infection in bat cell culture), examine the pathogenesis of these new viruses, and a pool of available bat viruses which **have not yet emerged in humans**. This multidisciplinary approach represents the first, concerted effort to understand the depth and breadth of the process of emergence within a key group of wildlife hosts associated with the recent emergence of SARS, Nipah, Hendra, Ebola and Marburg viruses.

<https://grantome.com/grant/NIH/R01-AI079231-02>

2009 The WIV began working with PREDICT, a new program established at USAID to train and fund scientists to test “high-risk” areas for new viruses. By identifying unknown viruses before they spilled over into humans—to “find them before they find us,” as **Shi Zhengli** put it—researchers hoped to establish an early-warning system. PREDICT worked in dozens of countries, but the WIV was one of its linchpins, and **Shi Zhengli** became famous as China’s “Bat Woman.”



H5N1 AVIAN FLU VIRUS

RON FOUCHIER, EARLY GAIN-OF-THREAT “SCIENTIST CREATED AN AVIAN FLU VIRUS THAT COULD INFECT HUMANS

2011 Ron Fouchier created an airborne Avian Flu virus that could infect humans. Baric “They created a virus like H5N1 which has a 50 percent mortality rate and they trained it how to be efficiently transmitted in mammals. And so that’s scary.” The virus, H5N1, causes bird flu, which rarely infects people but has an extraordinarily high death rate when it does. Since the virus was first detected in 1997, about 600 people have contracted it, and more than half have died. Nearly all have caught it from birds, and most cases have been in Asia. Scientists have watched the virus, worrying that if it developed the ability to spread easily from person to person, it could create one of the deadliest pandemics ever. A government advisory panel, the National Science Advisory Board for Biosecurity, overseen by the National Institutes of Health, has asked two journals, *Science* and *Nature*, to keep certain details out of reports that they intend to publish on the research. The panel said conclusions should be published, but not “experimental details and mutation data that would enable replication of the experiments.” **Dr. Anthony Fauci, head of the National Institute of Allergy and Infectious Diseases, said the research addressed important public health questions, but added, “I’m sure there will be some people who say these experiments never should have been done.” Dr. Fauci said staff members at the institutes followed the results of the research and flagged it as something that the biosecurity panel should evaluate.**

The potential for the modified H5N1 strain to cause a human pandemic if it ever slipped out of containment sparked sharp criticism. Rutgers molecular biologist Richard Ebright told *Science Magazine* that the research “should never have been done.” “When I first heard about the experiments that make highly pathogenic avian influenza transmissible,” says Philip Dormitzer, vice president and chief scientific officer of viral vaccines at Pfizer, “I was interested in the science but concerned about the risks of both the viruses

themselves and of the consequences of the reaction to the experiments."

<https://www.sciencemag.org/news/2011/11/scientists-brace-media-storm-around-controversial-flu-studies>

2011 or 2012 M.I.T. REPORTED: By taking thousands of samples from guano, fecal swabs, and bat tissue, and searching those samples for genetic sequences similar to SARS, Shi's team began to discover many closely related viruses. In a cave in Yunnan Province in 2011 or 2012, they discovered the two closest, which they named WIV1 and SHC014. Shi managed to culture WIV1 in her lab from a fecal sample and show that it could directly infect human cells, proving that SARS-like viruses ready to leap straight from bats to humans already lurked in the natural world. This showed, Daszak and Shi argued, that bat coronaviruses were a "substantial global threat." Scientists, they said, needed to find them, and study them, before they found us. Many of the other viruses couldn't be grown, but Baric's system provided a way to rapidly test their spikes by engineering them into similar viruses. When the chimera he made using SHC014 proved able to infect human cells in a dish, Daszak told the press that these revelations should "move this virus from a candidate emerging pathogen to a clear and present danger." To others, it was the perfect example of the unnecessary dangers of gain-of-function science. "The only impact of this work is the creation, in a lab, of a new, non-natural risk," the Rutgers microbiologist Richard Ebright, a longtime critic of such research, told Nature. To Baric, the situation was more nuanced. Although his creation might be more dangerous than the original mouse-adapted virus he'd used as a backbone, it was still wimpy compared with SARS—certainly not the supervirus Senator Rand Paul would later suggest. In the end, the NIH clampdown never had teeth. It included a clause granting exceptions "if head of funding agency determines research is urgently necessary to protect public health or national security." Not only were Baric's studies allowed to move forward, but so were all studies that applied for exemptions. The funding restrictions were lifted in 2017 and replaced with a more lenient system.

WORLD HEALTH ORGANIZATION IS IN FAVOR OF SHARING H5N1 VIRUS GAIN-OF-FUNCTION / GAIN-OF-THREAT RESEARCH

2011 "The World Health Organization has expressed concern that US attempts to block publication of aspects of recent research on the **H5N1** avian influenza virus may undermine an international agreement on sharing information on the virus. **The research relates to genetic mutations that might increase the virus's risk of transmission to humans.** W.H.O. raised its concerns in a statement released on **December 30, 2011** and urged that information gathered through such research be shared in the manner delineated in its pandemic influenza preparedness (PIP) framework which came into effect in May 2011."

<https://www.bmj.com/content/344/bmj.e30> (Published 04 January 2012)

W.H.O. CONCERNED THAT NEW H5N1 INFLUENZA RESEARCH COULD UNDERMINE THE 2011 PANDEMIC INFLUENZA PFREPREAREDNESS FRAMEWORK

December 30, 2011 "The World Health Organization (WHO) takes note that studies undertaken by several institutions on whether changes in the H5N1 influenza virus can make it more transmissible between humans have raised concern about the possible risks and misuses associated with this research. W.H.O. is also deeply concerned about the potential negative consequences. However, W.H.O. also notes that studies conducted under appropriate conditions must continue to take place so that critical scientific knowledge needed to reduce the risks posed by the H5N1 virus continues to increase."

http://www.who.int/mediacentre/news/statements/2011/pip_framework_20111229/en/index.html

THE PAPER DESCRIBING HOW THE LETHAL H5N1 BIRD FLU COULD BE MADE EASIER TO SPREAD WAS PUBLISHED SIX MONTHS AFTER A SCIENTIFIC ADVISORY BOARD SUGGESTED THAT THE PAPERS' MOST POTENTIALLY DANGEROUS DATA BE CENSORED.

JUNE 21, 2012 The paper, by scientists at Erasmus Medical Center in the Netherlands, identified five mutations apparently necessary to make the bird flu virus spread easily among ferrets, which catch the same flus that humans do. **"There is always a risk," Dr. Anthony S. Fauci, the director of the National Institute for Allergy and Infectious Diseases, said in a telephone news conference held by "But I believe the benefits are greater than the risks."** Two of the five mutations are already common in the H5N1 virus in the wild, said Ron A. M. Fouchier, the paper's lead author. One mutation has been found in H5N1 only once. The remaining two have never been found in wild H5N1, but occurred in the H2 and H3 flus that caused the 1957 Asian flu pandemic and the 1968 Hong Kong flu. **The Dutch team artificially introduced three mutations. The last two occurred as the virus was "passaged" through 10 generations of ferrets by using nasal washes from one to infect the next. Four changes were in the hemagglutinin "spike" that attaches the virus to cells. The last was in the PB2 protein. As the virus became more contagious, it lost lethality. It did not kill the ferrets that caught it through airborne transmission, but it did kill when high doses were squirted into the animals' nostrils. Dr. Fouchier's work proved that H5N1 need not mix with a more contagious virus to become more contagious. Asked if a rogue researcher could now try to duplicate Dr. Fouchier's work, Dr. Fauci said it was possible. But he argued that open discussion was still better than restriction to a few government-cleared flu researchers, because experts in unrelated fields, like X-ray crystallography or viral epidemiology, might take interest and eventually make important contributions, he said. "Being in the free and open literature makes it easier to get a lot of the good guys involved than the risk of getting the rare bad guy involved," Fauci said.**

<https://www.nytimes.com/2012/06/22/health/h5n1-bird-flu-research-that-stoked-fears-is-published.html>

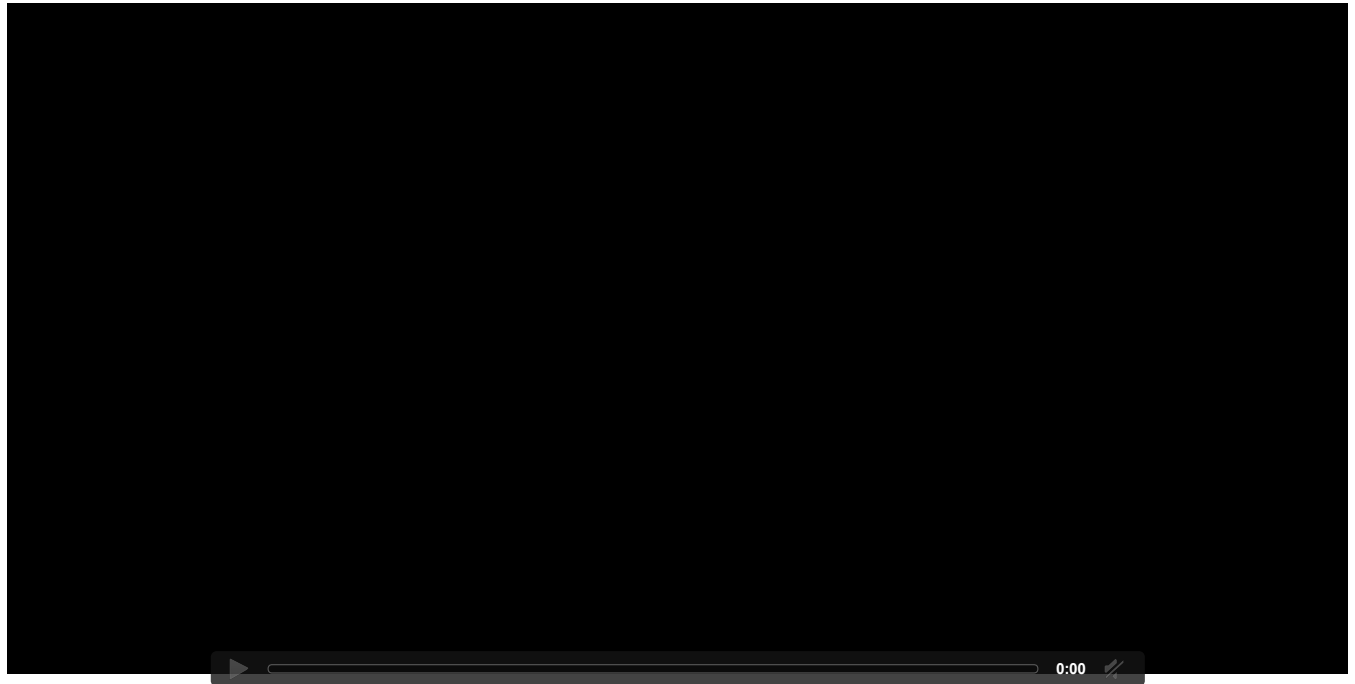
FOUCHIER EXPLAINED HOW EASY IT WAS TO CREATE AN AIRBORNE AVIAN FLU VIRUS THAT COULD INFECT HUMANS USING GAIN-OF-THREAT TECHNOLOGY



"Flu viruses are basically eight pieces of RNA wrapped up in a ball. To create the gain-of-threat mutations, use a DNA template for each piece, called a plasmid. Making a single mutation in the plasmid is easy and it's commonly done in genetics labs. If you insert all eight plasmids into a mammalian cell, they hijack the cell's machinery to create flu virus RNA. Now you can start to assemble a new virus particle in that cell. One infected cell is enough to grow many new virus particles — from one to a thousand to a million; viruses are replication machines. And because they mutate so readily during their replication, the new viruses have to be checked to make sure it only has the mutations the lab caused. The virus then goes into the ferrets, passing through them to generate new viruses until, on the 10th generation, it infected ferrets through the air. By analyzing the virus's genes in each generation, one can figure out what exact five mutations lead to **H5N1** bird flu being airborne between ferrets."

US-CHINA ECOLOGY AND EVOLUTION OF INFECTIOUS DISEASES COLLABORATIVE WORKSHOP; KUNMING, CHINA

OCTOBER 2012 This award supports a workshop that will explore the potential for in the area of ecology and evolution of infectious diseases. The workshop be held in Kunming China in October 2012. Investigators from the United States and China will discuss research priorities and ways to collaborate and explore the potential for joint US and China research in the area of ecology and



2013 The WIV discovered SARS-CoV, the cause of SARS, in a cave in Yunnan Province. **SHI ZHENGLI** team found that the bats of southern China were full of viruses, especially coronaviruses. Over 10 years, her team collected more than 10,000 samples from bats in the region and discovered hundreds of new coronaviruses, including some with the ability to infect humans. Many bats harbored multiple viruses, and there were alarming signs that the viruses were recombining with each other—swapping chunks of genetic code as they replicated, producing novel viruses with new abilities.

BATS AS ANIMAL RESERVOIRS FOR THE SARS CORONAVIRUS: HYPOTHESIS PROVED AFTER 10 YEARS OF VIRUS HUNTING VIROLOGICA SINICA

OCTOBER 30, 2013 Recently, the team led by Dr. Zhengli Shi from Wuhan Institute of Virology, Chinese Academy of Sciences, and Dr. Peter Daszak from Ecohealth Alliance identified SL-CoVs in Chinese horseshoe bats that were 95% identical to human SARS-CoV and were able to use human Angiotensin-Converting Enzyme 2 (**ACE2**) receptor for docking and entry. Remarkably, they isolated the first known live bat SL-CoV that replicates in human and related cells. Their findings provide clear evidence that some SL-CoVs circulating in bats are capable of infecting and replicating in human cells

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7091109>

NIAD AND HIH GRANTS

2014 EcoHealth Alliance received a \$3.4 million grant from the National Institute of Allergy and Infectious Diseases in 2014, which the nonprofit used, working with its Wuhan institute collaborators, to study coronaviruses in **bats roosting in caves in China and how the viruses infect people**. <https://www.wsj.com/articles/nih-presses-u-s-nonprofit-for-information-on-wuhan-virology-lab-11597829400>

Brand-new pathogens. In 2014, the NIH awarded a five-year, \$3.75 million grant to EcoHealth Alliance to study the risk that more bat-borne coronaviruses would emerge in China, using the same kind of Gain-of-Threat techniques Baric had pioneered. Some of that work was to be subcontracted to the Wuhan Institute of Virology. (MIT Tech Review)

ONE OF SEVERAL NEAR FATAL ERRORS THAT TRIGGERED THE GoF / GOT BAN INVOLVED H5N1 INFLUENZA VIRUS

JULY 11, 2014 "After potentially serious back-to-back laboratory accidents, federal health officials announced that they had temporarily closed the flu and anthrax laboratories at the Centers for Disease Control and Prevention in Atlanta and halted shipments of all infectious agents from the agency's highest-security labs. In one episode, at least 62 C.D.C. employees may have been exposed to live anthrax bacteria after potentially infectious samples were sent to laboratories unequipped to handle them. Employees not wearing protective gear worked with bacteria that were supposed to have been killed but may not have been. All were offered a vaccine and antibiotics, and the agency said it believed no one was in danger. In a second accident, a C.D.C. lab accidentally contaminated a relatively benign flu sample with a dangerous H5N1 bird flu strain that has killed 386 people since 2003. Fortunately, a United States Agriculture Department laboratory realized that the strain was more dangerous than expected and alerted the C.D.C. Two of six vials of smallpox recently found stored in a National Institutes of Health laboratory since 1954 contained live virus capable of infecting people.

<https://www.nytimes.com/2014/07/12/science/cdc-closes-anthrax-and-flu-labs-after-accidents.html>

"As this report was being finalized, CDC leadership was made aware that earlier this year a culture of lowpathogenic avian influenza was unintentionally cross-contaminated at a CDC influenza laboratory with a highly pathogenic **H5N1** strain of influenza and shipped to a BSL-3, select-agent laboratory operated by the United States Department of Agriculture (USDA). The CDC influenza laboratory where this incident occurred is now closed and will not reopen until adequate improvements are put in place. Although CDC is continuing to investigate and review this matter, Attachment A provides current information on the incident and the agency's response."¹

https://www.cdc.gov/labs/pdf/Final_Anthrax_Report.pdf

1. COMMENT: Most of these accidents involved the shipment of live anthrax bacteria initially believed to be inactivated exposed lab technicians to contamination.

OBAMA BANS GAIN-OF-FUNCTION / GAIN-OF-THREAT RESEARCH IN US

In **OCTOBER 2014** in response to researchers' fears and some lab incidents, the federal government imposed a moratorium on all Gain-of-Function / Gain-of-Threat research, freezing the work.

<https://www.freethink.com/articles/gain-of-function-mutation>



DOING DILIGENCE TO ASSESS THE RISKS AND BENEFITS OF LIFE SCIENCES GAIN-OF-FUNCTION RESEARCH

OCTOBER 17, 2014 "Summary: The White House Office of Science and Technology Policy and Department of Health and Human Services today announced that the U.S. Government is launching a deliberative process to assess the potential risks and benefits associated with a subset of life sciences research known as gain-of-function studies."

<https://obamawhitehouse.archives.gov/blog/2014/10/17/doing-diligence-assess-risks-and-benefits-life-sciences-gain-function-research>

OCTOBER 2014 Gain-of-Function / Gain-of-Threat studies, **or research that improves the ability of a pathogen to cause disease**, help define the fundamental nature of human-pathogen interactions, thereby enabling assessment of the pandemic potential of emerging infectious agents, informing public health and preparedness efforts, and furthering medical countermeasure development. Gain-of-Function / Gain-of-Threat studies may entail biosafety and biosecurity risks; therefore, the risks and benefits of Gain-of-Function / Gain-of-Threat research must be evaluated, both in the context of recent U.S. biosafety incidents and to keep pace with new technological developments, in order to determine which types of studies should go forward and under what conditions. **In light of recent concerns regarding biosafety and biosecurity, effective immediately, the U.S. Government (USG) will pause new USG funding for gain-of-function / gain-of-threat research on influenza, MERS or SARS viruses, as defined below. This research funding pause will be effective until a robust and broad deliberative process is completed that results in the adoption of a new USG Gain-of-Function research policy.** Restrictions on new funding will apply as follows: New USG funding will not be released for gain-of-function research projects that may be reasonably anticipated to confer attributes to influenza, MERS, or SARS viruses such that the virus would have enhanced pathogenicity and/or transmissibility in mammals via the respiratory route. The research funding pause would not apply to characterization or testing of naturally occurring influenza, MERS, and SARS viruses, unless the tests are reasonably anticipated to increase transmissibility and/or pathogenicity." <http://www.phe.gov/s3/dualuse/Documents/gain-of-function.pdf>

GAIN-OF-FUNCTION / GAIN-OF-THREAT OUTSOURCED TO WUHAN INSTITUTE OF VIROLOGY AFTER AMERICA BANS IT AS TOO DANGEROUS

2014-2019 *Daily Mail*: "The US National Institutes of Health (NIH) funded bat-coronavirus research in the Wuhan Institute of Virology in China to the tune of US\$3.7 million. Back in October 2014, the US government had placed a federal moratorium on gain-of-function (GoF) research – altering natural pathogens to make them more deadly and infectious – as a result of rising fears about a possible pandemic caused by an accidental or deliberate release of these genetically engineered monster germs.¹ A portion of \$3.7 million in grants awarded between 2014 and 2019 by the National Institutes of Health (NIH) funded research at the Wuhan Institute of Virology in China. However, not all of that \$3.7 million went to the WIV, and not all of the funding took place under the Obama administration. Approximately \$700,000 of the \$3.7 million total was approved under Donald Trump."

<https://asiatimes.com/2020/04/why-us-outsourced-bat-virus-research-to-wuhan>

<https://www.snopes.com/fact-check/obama-admin-wuhan-lab-grant>

1. The funding was laundered through Daszak's ECOHEALTH ALLIANCE.

UNDERSTANDING THE RISK OF BAT CORONAVIRUS EMERGENCE (DASZAK)

JUNE 1, 2014 "Develop predictive models of bat CoV emergence risk and host range. A combined modeling approach will include phylogenetic analyses of host receptors and novel CoV genes (including functional receptor binding domains); a fused ecological and evolutionary model to predict host-range and viral sharing; and mathematical matrix models to examine evolutionary and transmission dynamics. Test predictions of CoV inter-species transmission. **Predictive models of host range (i.e. emergence potential) will be tested experimentally using reverse genetics, pseudovirus and receptor binding assays, and virus infection experiments across a range of cell cultures from different species and humanized mice.**" <https://grantome.com/grant/NIH/R01-AI110964-04>

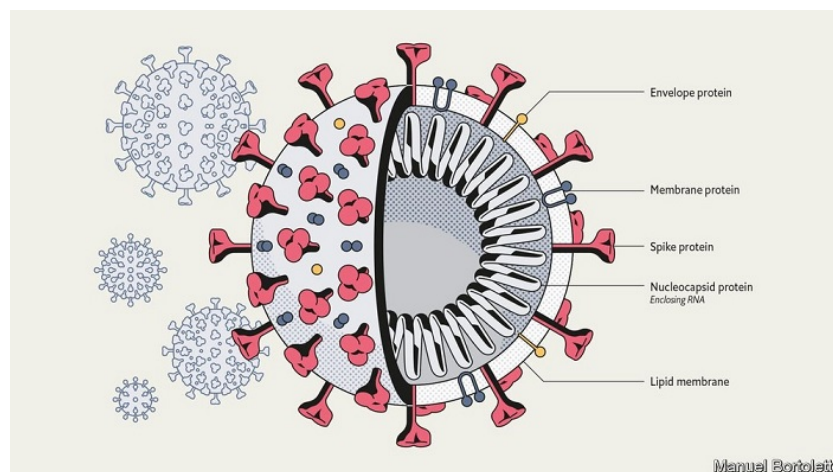
Project Start
2014-06-01
Project End
2019-05-31

Budget Start
2017-06-01
Budget End
2018-05-31
Support Year
4
Fiscal Year
2017
Total Cost
\$597,112
Indirect Cost¹
\$121,096

1. This is the money sent to the WIV

IN VITRO AND IN VIVO CHARACTERIZATION OF SARSr-COV SPILLOVER RISK, COUPLED WITH SPATIAL AND PHYLOGENETIC ANALYSES TO IDENTIFY THE REGIONS AND VIRUSES OF PUBLIC HEALTH CONCERN (DASZAK)

JUNE 6, 2014 "We will use **Spike Protein sequence data**,¹ **infectious clone technology**,² **in vitro and in vivo infection experiments and analysis of receptor binding** to test the hypothesis that % divergence thresholds in **Spike Protein** sequences predict spillover potential. We will combine these data with bat host distribution, viral diversity and phylogeny, human survey of risk behaviors and illness, and serology to identify SARSr-CoV spillover risk hotspots **across southern China**. Together these data and analyses will be critical for the future development of public health interventions and enhanced surveillance to prevent the re-emergence of SARS or **the emergence of a novel SARSr-CoV**. Project Start 2014-06-01 / Project End 2020-04-24 / Budget Start 2019-07-24 / Budget End 2020-04-24 / Support Year 6 / Fiscal Year 2019 / Total Cost / Indirect Cost"
<https://grantome.com/grant/NIH/R01-AI110964-06>



1. The features that make SARS-CoV-2 more deadly include insertions of specific stretches of amino acids into two virus proteins, the nucleocapsid and the spike...In particular, the insertions in the spike protein are predicted, from protein structure analysis, to facilitate the recognition of the coronavirus receptors on human cells and the subsequent penetration of the virus into those cells. Finding these features in animal coronavirus isolates could predict the jump to humans and the severity of disease caused by such isolates.

<https://www.nih.gov/news-events/news-releases/nih-researchers-identify-key-genomic-features-could-differentiate-sars-cov-2-other-coronaviruses-cause-less-severe-disease>

JUNE 6, 2014 1R01 A1110964 Daszak(PI) 06/01/14-05/31/19 Understanding the Risk of Bat Coronavirus Emergence The goal of this work is to conduct ecological and virological studies on bats in China that harbor SARS-like coronaviruses, and conduct behavioral risk surveys and testing in people, with a goal of identifying risk factors for further spillover of SARS-like Co Vs, and help identify the likely drivers of the SARS-CoV outbreak in 2003. [INTERCEPT Page 26](#)

METHODS AND COMPOSITIONS FOR CHIMERIC CORONAVIRUS SPIKE PROTEINS (BARIC)

MARCH 20, 2015 "In one aspect, the present invention provides a **chimeric coronavirus spike protein** comprising, in orientation from amino to carboxy terminus: a) a first region comprising a portion of a coronavirus **Spike Protein** ectodomain that precedes the receptor binding domain (RBD) as located in a nonchimeric coronavirus spike protein, of a first coronavirus; b) a second region comprising a coronavirus **Spike Protein** receptor binding domain (RBD) of a second coronavirus that is different from said first coronavirus; c) a third region comprising a portion of a coronavirus **Spike Protein** S1 domain as located in a nonchimeric coronavirus **Spike Protein** immediately downstream of the RBD, contiguous with a portion comprising a coronavirus spike protein S2 domain as located immediately upstream of a fusion protein domain in a nonchimeric coronavirus **Spike Protein**, wherein said third region is of said first coronavirus; and d) a fourth region comprising a portion of a coronavirus **Spike Protein** from the start of the fusion protein domain through the carboxy terminal end as located in a nonchimeric coronavirus spike protein of a third coronavirus that is different from said first coronavirus and said second coronavirus. <https://patents.justia.com/patent/9884895>

The **Spike Protein (S)** of SARS-CoV-2, which plays a key role in the receptor recognition and cell membrane fusion process, is composed of two subunits, S1 and S2. The S1 subunit contains a receptor-binding domain that recognizes and binds to the host receptor Angiotensin-Converting Enzyme 2, **ACE2** while the S2 subunit mediates viral cell membrane fusion by forming a six-helical bundle via the two-heptad repeat domain. In this review, we highlight recent research advance in the structure, function and development of antiviral drugs targeting the (S).

A large number of glycosylated **Spike Proteins** cover the surface of SARS-CoV-2 and bind to the host cell receptor Angiotensin-Converting Enzyme 2 (**ACE2**), mediating viral cell entry. When the **Spike Protein** binds to the receptor, TM protease serine 2 (TMPRSS2), a type 2 TM serine protease located on the host cell membrane, promotes virus entry into the cell by activating the

Spike Protein. Once the virus enters the cell, the viral RNA is released, polyproteins are translated from the RNA genome, and replication and transcription of the viral RNA genome occur via protein cleavage and assembly of the replicase–transcriptase complex. Viral RNA is replicated, and structural proteins are synthesized, assembled, and packaged in the host cell, after which viral particles are released."



It is obvious that Daszak and his associates were experimenting with S1 and S2 SARS proteins and its coupling with the ACE2 receptors making them fit like a plug in an AC outlet and increasing their infectivity.

SILLOVER AND PANDEMIC PROPERTIES OF ZOONOTIC VIRUSES WITH HIGH HOST PLASTICITY (DASZAK)

OCTOBER 2015 Zoonotic virus spillover from wildlife was most frequent in and around human dwellings and in agricultural fields, as well as at interfaces with occupational exposure to animals (hunters, laboratory workers, veterinarians, researchers, wildlife management, zoo and sanctuary staff). Primate hosts were most frequently cited as the source of viruses transmitted by direct contact during hunting and in laboratories, while rodent hosts were more likely to be implicated in transmission by indirect contact in and around human dwellings and in agricultural fields. <https://www.nature.com/articles/srep14830>

SARS-LIKE WIV1-COV POISED FOR HUMAN EMERGENCE / SHI ZHENGLI AND BARIC CO-AUTHORS



Published in final edited form as:
Nat Med. 2015 December ; 21(12): 1508–1513. doi:10.1038/nm.3985.

SARS-like cluster of circulating bat coronavirus pose threat for human emergence

Vineet D. Menachery¹, Boyd L. Yount Jr¹, Kari Debbink^{1,2}, Sudhakar Agnihothram³, Lisa E. Gralinski¹, Jessica A. Plante¹, Rachel L. Graham¹, Trevor Scobey¹, Xing-Yi Ge⁸, Eric F. Donaldson¹, Scott H. Randell^{4,5}, Antonio Lanzavecchia⁶, Wayne A. Marasco⁷, Zhengli-Li Shi⁹, and Ralph S. Baric^{1,2}

NOVEMBER 9, 2015 Two Wuhan Institute of Virology scientists, Xing-Yi Ge and **Shi Zhengli**, use reverse genetics to generate a chimeric virus (one that has been created by combining cells of more than one distinct genotype) closely resembling the novel coronavirus Covid-19: **"On the basis of these findings, we synthetically re-derived an infectious full-length SHC014 recombinant virus and demonstrate robust viral replication both in vitro and in vivo."** The *Nature Medicine* article also mentions, "Human lungs for HAE cultures were procured under University of North Carolina at Chapel Hill Institutional Review Board–approved protocols." **Shi joined with an American researcher, Ralph Baric of University of North Carolina**, to generate an **artificial coronavirus (a chimera), SHC014-MA15, by recombining a SARS coronavirus extracted from an infected mouse as backbone and a section of genome representing the Spike Protein of the SARS-like coronavirus, SHC014, which Shi's colleague found in 2012.** This chimera were tested in vitro (test tube) and in vivo (live animals) and showed that it was capable of viral replication and could cause "robust refection to human airway culture and mice, particularly aggressive to **aged mice."** *Hong Kong Chinese News* JUNE 2021: "Those 50 and older continue to make up the bulk of Covid-19 deaths. Among that cohort, white Americans are driving the shifts in death patterns. At the height of the pandemic, those who were white and aged 75 and older accounted for more than half of all Covid-19 deaths. Now, they make up less than a third." **NYT**

To examine the emergence potential (that is, the potential to infect humans) of circulating bat CoVs, we built a chimeric virus encoding a novel, zoonotic CoV spike protein—from the RsSHC014-CoV sequence that was isolated from Chinese horseshoe bats¹—in the context of the SARS-CoV mouse-adapted backbone. The hybrid virus allowed us to evaluate the ability of the novel spike protein to cause disease independently of other necessary adaptive mutations in its natural backbone. Using this approach, we characterized CoV infection mediated by the SHC014 spike protein in primary human airway cells and in vivo, and tested the efficacy of available immune therapeutics against SHC014-CoV. Together, the strategy translates metagenomics data to help predict and prepare for future emergent viruses. <https://www.nature.com/articles/nm.3985>

OXFORD UNIVERSITY PUBLICATION NATURE "ENGINEERED BAT VIRUS STIRS DEBATE OVER RISKY RESEARCH: LAB-MADE CORONA VIRUS RELATED TO SARS CAN INFECT HUMAN CELLS"



November 12, 2015 "Declan Butler: An experiment that created a **hybrid version of a bat coronavirus** — one related to the virus that causes SARS (severe acute respiratory syndrome) — has triggered renewed debate over whether engineering lab variants of viruses with possible pandemic potential is worth the risks. In an article published in *Nature Medicine*¹ on November 9, 2015, scientists investigated a virus called **SHC014**, which is



found in horseshoe bats in China. The researchers created a chimaeric virus, made up of a surface protein of SHC014 and the backbone of a SARS virus that had been adapted to grow in mice and to mimic human disease. The chimaera infected human airway cells — proving that the surface protein of SHC014 has the necessary structure to bind to a key receptor on the cells and to infect them. It also caused disease in mice, but did not kill them. Although almost all coronaviruses isolated from bats have not been able to bind to the key human receptor, **SHC014**, is not the first that can do so. In 2013, researchers reported this ability for the first time in a different coronavirus isolated from the same bat population. The findings reinforce suspicions that bat coronaviruses capable of directly infecting humans (rather than first needing to evolve in an intermediate animal host) may be more common than previously thought, the researchers say. But other virologists question whether the information gleaned from the experiment justifies the potential risk. Although the extent of any risk is difficult to assess, Simon Wain-Hobson, a virologist at the Pasteur Institute in Paris, points out that the researchers have created a novel virus that “grows remarkably well” in human cells. **“If the virus escaped, nobody could predict the trajectory,”** he says.

THE ARGUMENT IS ESSENTIALLY A RERUN OF THE DEBATE OVER WHETHER TO ALLOW LAB RESEARCH THAT INCREASES THE VIRULENCE, EASE OF SPREAD OR HOST RANGE OF DANGEROUS PATHOGENS — WHAT IS KNOWN AS ‘GAIN-OF-FUNCTION’ RESEARCH.

November 12, 2015 In October 2014, the US government imposed a moratorium on federal funding of such research on the viruses that cause **SARS**, influenza and MERS (Middle East respiratory syndrome, a deadly disease caused by a virus that sporadically jumps from camels to people). The latest study was already under way before the US moratorium began, and the US National Institutes of Health (NIH) allowed it to proceed while it was under review by the agency, says **Ralph Baric**, an infectious-disease researcher at the University of North Carolina at Chapel Hill, a co-author of the study. The NIH eventually concluded that the work was not so risky as to fall under the moratorium, he says. But Wain-Hobson disapproves of the study because, he says, it provides little benefit, and reveals little about the risk that the wild SHC014 virus in bats poses to humans.” <https://www.nature.com/news/engineered-bat-virus-stirs-debate-over-risky-research-1.18787>

DECEMBER 2015 The emergence of Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) and Middle East Respiratory Syndrome (MERS)-CoV underscores the threat of cross-species transmission events leading to outbreaks in humans. In this study, we examine the disease potential for SARS like CoVs currently circulating in **Chinese horseshoe bat populations**. **Utilizing the SARS-CoV infectious clone, we generated and characterized a chimeric virus expressing the spike of bat coronavirus SHC014 in a mouse adapted SARS-CoV backbone. The results indicate that group 2b viruses encoding the SHC014 spike in a wild type backbone can efficiently utilize multiple ACE2 receptor orthologs, replicate efficiently in primary human airway cells, and achieve in vitro titers equivalent to epidemic strains of SARS-CoV.** Additionally, in vivo experiments demonstrate replication of the chimeric virus in mouse lung with notable pathogenesis. Evaluation of available SARS-based immune-therapeutic and prophylactic modalities revealed poor efficacy; both monoclonal antibody and vaccine approaches failed to neutralize and protect from CoVs utilizing the novel spike protein. Importantly, based on these findings, we synthetically rederived an infectious full length SHC014 recombinant virus and demonstrate robust viral replication both in vitro and in vivo. Together, the work highlights a continued risk of SARS-CoV reemergence from viruses currently circulating in bat populations [SARS-LIKE-CLUSTER-OF-CIRCULATING-BAT-CORONAVIRUSES-SHOWS-POTENTIAL-FOR-HUMAN-EMERGENCE](#)

2015 ISOLATION AND CHARACTERIZATION OF A NOVEL BAT CORONA VIRUS CLOSELY RELATED TO THE DIRECT PROGENITOR OF SEVERE ACUTE RESPIRATORY SYNDROME CORONAVIRUS

DECEMBER 29, 2015 Yang XL1, Hu B1, Wang B1, Wang MN1, Zhang Q1, Zhang W1, Wu LJ1, Ge XY1, Zhang YZ2, **PETER DASZAK P3**, Wang LF4, **SHI ZHENGLI** ZL5 Author information [All worked at Wuhan Institute of Virology] *Journal of Virology*, **Dec 29, 2015**, 90(6):3253-3256 DOI: 10.1128/JVI.02582-15 PMID: 26719272 PMCID: PMC4810638 NIAID NIH HHS (2)? Grant ID: R01 / AI110964 19 publications Grant ID: R01AI110964 3 publications Google search of Grant ID: R01AI110964 takes us to [NIH: National Institute of Allergy and Infectious Diseases \(Dr. FAUCI\)](#)

“We report the isolation and characterization of a novel bat coronavirus which is much closer to the severe acute respiratory syndrome coronavirus (SARS-CoV) in genomic sequence than others previously reported, particularly in its **S gene**. Cell entry and susceptibility studies indicated that this virus can use **ACE2** as a receptor and infect animal and human cell lines. Our results provide further evidence of the bat origin of the SARS-CoV and highlight the likelihood of future bat coronavirus emergence in humans.” We recently isolated a bat SL-CoV-1 strain (WIV1) and **constructed an infectious clone** of another strain (SHC014); significantly, these strains are closely related to SARS-CoV and capable of using the same cellular receptor (angiotensin-converting enzyme 2 [ACE2] as SARS-CoV-1. Despite the high similarity in genomic sequences and receptor usage of these two strains, there is still some difference between the N-terminal domains of the **S proteins** of SARS-CoV-1 and other SL-CoVs, indicating that other unknown SL-CoV-1s are circulating in bats.” <https://europepmc.org/article/pmc/pmc4810638>

“In **2016** MIT: Daszak and Shi published a paper reporting how the Chinese lab had engineered different versions of WIV1 and tested their infectiousness in human cells. The paper announced that the WIV had developed its own reverse-genetics system, following the Americans’ lead. It also included a troubling detail: the work, which was funded in part by the NIH grant, had been done in a BSL-2 lab. That meant the same viruses that Daszak was holding up as a clear and present danger to the world were being studied under conditions that, according to Richard Ebright, matched “the biosafety level of a US dentist’s office.” Ebright believes one factor at play was the cost and inconvenience of working in high-containment conditions. The Chinese lab’s decision to work at BSL-2, he says, would have “effectively increas[ed] rates of progress, all else being equal, by a factor of 10 to 20”—a huge edge. Work at the WIV was indeed progressing quickly. In 2017, Daszak and Shi followed with another study, also at BSL-2, that one-upped Baric’s work in North Carolina. The WIV had continued to unearth dozens of new SARS-like coronaviruses in bat caves, and it reported making chimeras with eight of them by fusing the spikes of the new viruses to the chassis of WIV1. Two of them replicated well in human cells. They were, for all intents and purposes, brand-new pathogens. The revelation that the WIV was working with SARS-like viruses in subpar safety conditions has led some people to reassess the chance that SARS-CoV-2 could have emerged from some type of laboratory incident. “That’s screwed up,” the Columbia University virologist Ian Lipkin, who coauthored the seminal paper arguing that covid must have had a natural origin, told the journalist Donald McNeil Jr. “It shouldn’t have happened. People should not be looking at bat viruses in BSL-2 labs. My view has changed.”

But the WIV was not breaking any rules by working at BSL-2, says Filippa Lentzos, a biosecurity expert at King’s College London “There are no enforceable standards of what you should and shouldn’t do. It’s up to the individual countries, institutions, and scientists.” And in China, she says, the vertiginous rise of high-tech biological research has not been accompanied by an equivalent increase in oversight. In an email, Zhengli Shi said she followed Chinese rules that are similar to those in the US. Safety requirements are based on what virus you are studying. Since bat viruses like WIV1

haven't been confirmed to cause disease in human beings, her biosafety committee recommended BSL-2 for engineering them and testing them and BSL-3 for any animal experiments. In response to questions about the decision to do the research in BSL-2 conditions, Peter Daszak forwarded a statement from EcoHealth Alliance stating that the organization "must follow the local laws of the countries in which we work" and that the NIH had determined the research was "not gain-of-function."

EARLY 2016 Shi sent Baric a fresh bat virus **Spike Protein**, and Baric inserted it into the backbone of a human SARS virus and then used that **infectious clone** to attack human airway cells.

MARCH 14, 2016 The emergence of Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) and Middle East respiratory syndrome (MERS)-CoV highlights the continued risk of cross-species transmission leading to epidemic disease. This manuscript describes efforts to extend surveillance beyond sequence analysis, **constructing chimeric and full-length zoonotic coronaviruses to evaluate emergence potential. Focusing on SARS-like virus sequences isolated from Chinese horseshoe bats, the results indicate a significant threat posed by WIV1-CoV. Both full-length and chimeric WIV1-CoV readily replicated efficiently in human airway cultures and in vivo, suggesting capability of direct transmission to humans.** In addition, while monoclonal antibody treatments prove effective, the SARS-based vaccine approach failed to confer protection. Together, the study indicates an ongoing threat posed by WIV1-related viruses and the need for continued study and surveillance. **"The virus readily and efficiently replicated in cultured human airway tissues, suggesting an ability to potentially jump directly to humans," reported the University of North Carolina [Baric] website. This time, they also used the bat-human hybrid virus to infect transgenic humanized mice that grew human ACE2 protein. The mice, young and old, lost weight and died, proving, again, that this particular bat virus was potentially "poised to emerge in human populations."** It was "an ongoing threat," Baric wrote. <https://www.pnas.org/content/113/11/3048>

A REPORT OF THE NATIONAL SCIENCE ADVISORY BOARD FOR BIOSECURITY RECOMMENDATIONS FOR THE EVALUATION AND OVERSIGHT OF PROPOSED GAIN-OF-FUNCTION RESEARCH

THIS REPORT IS CRITICAL OF GOF

MAY 2016 This report further defines "gain-of function research of concern" to describe the subset of studies that have been the subject of recent debate and have raised potential biosafety and biosecurity implications. These are gain-of function studies **with the potential to generate pathogens with pandemic potential in humans by exhibiting high transmissibility and high virulence.** The RBA (RISK AND BENEFIT ASSESSMENTS) contains a number of other useful analyses as well, including background and contextual information on the biology of influenza and **coronavirus**, historical analysis of naturally-occurring seasonal and pandemic influenza and **coronavirus outbreaks**, an examination of the potential proliferation of GOF research, **and analysis of the potential loss of public trust in science that could result if a laboratory incident involving GOF research were to occur.** The biosecurity risk assessment shows that the most probable threats involve insiders who have direct access to dangerous pathogens or **outsiders [Daszak] who collaborate with or subvert insiders.**

In addition to the agents and toxins on the list, the select agent regulations apply to some genetic elements, including nucleic acids that are immediate precursors to infectious forms of any select agent viruses (i.e., complete positive strand RNA viral genomes), as well as some nucleic acids that encode select toxins. [Baric's experiments bringing extinct viruses back to life.] Select agent regulations also apply to genetically-modified select agents and toxins. Restricted experiments are described in the regulations and involve the deliberate transfer of or selection for a drug resistance trait to select agents that are not known to acquire the trait naturally.

As with all life sciences research involving pathogens, GOF studies entail inherent biosafety and biosecurity risks. GOF research involving the generation of pathogens with pandemic potential involves the greatest risks. A laboratory accident involving such a pathogen could potentially release a pathogen that could spread rapidly and efficiently through the human population.

Manipulations that increase transmissibility, increase pathogenicity, and enable a pathogen to more readily spread through the population have the greatest potential to increase risk; in some strains even a moderate increase might be a concern...GOFROC entails the generation of pathogens—perhaps novel pathogens—with anticipated pandemic potential. The risks associated with such studies are uncertain but potentially significant. **It is possible that generating a laboratory pathogen with pandemic potential introduces a risk of a pandemic, albeit a low probability risk, that did not exist before that pathogen was generated...The pathogen generated is likely highly transmissible and likely capable of wide and uncontrollable spread in human populations. To be considered "highly transmissible" the pathogen must be judged to have the capacity for sustained secondary transmission among humans, particularly, but not exclusively, by the respiratory route.**

Importantly, a proposed experiment need not involve the simultaneous enhancement of both phenotypes. Thus, research involving a naturally-occurring pathogen that exhibits one of the above attributes would be considered GOFROC if a study were anticipated to confer the second attribute to the agent (while retaining the first attribute). Other studies may generate a pathogen with the above attributes after a series of manipulations that enhance the phenotypes separately but ultimately result in a pathogen with both attributes. Any route of experimentation that is anticipated to ultimately generate a pathogen that exhibits both of the characteristics above would be considered GOFROC [Gain-of-Function Research of Concern] and should be reviewed carefully before it can be funded. Pathogen characteristics recommended for consideration in the RA (RISK ASSESSMENT) and BA (BENEFIT ASSESSMENT) **The RA and BA should include analysis of the risks and benefits associated with GoF experiments that are anticipated to increase the pandemic potential of pathogens.** Toward this end, the following characteristics, which may be conferred to pathogens during the conduct of GoF studies, should be considered:

- 1. Enhanced pathogen production as a result of changes in the replication cycle or growth.
- 2. Enhanced morbidity and mortality in appropriate animal models.
- 3. Enhanced transmission in mammals (e.g., increased host or tissue range, altered route of transmission, infectivity above a certain threshold determined in an appropriate animal model).
- 4. Evasion of existing natural or induced immunity.
- 5. Resistance to drugs or evasion of other medical countermeasures such as **vaccines**, therapeutics, diagnostics.

[NSABB_Final_Report_Recommendations_Evaluation_Oversight_Proposed_Gain_of_Function_Research.pdf](#)

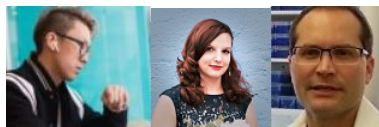
Scientists who were far more educated and experienced than the mere Zoologist Daszak knew the potential was there to cause a pandemic. But Daszak had an agenda so he made sure they continued.

BAT SEVERE ACUTE RESPIRATORY SYNDROME-LIKE CORONAVIRUS WIV1 ENCODES AN EXTRA ACCESSORY PROTEIN, ORFX, INVOLVED IN MODULATION OF THE HOST IMMUNE RESPONSE (BARIC, SHI ZHENGLI)

NOVEMBER 2016 ABSTRACT: Bats harbor severe acute respiratory syndrome (SARS)-like coronaviruses (SL-CoVs) from which the causative agent of the 2002-2003 SARS pandemic is thought to have originated. However, despite the fact that a large number of genetically diverse SL-CoV sequences have been detected in bats, only two strains (named WIV1 and WIV16) have been successfully cultured in vitro. These two strains differ from SARS-CoV only in containing an extra Open Reading Frame (ORF) (named ORFX), between ORF6 and ORF7, which has no homology to any known protein sequences. **In this study, we constructed a full-length cDNA clone of SL-CoV WIV1 (rWIV1), an ORFX deletion mutant (rWIV1-X), and a Green Fluorescent Protein (GFP)¹-expressing mutant (rWIV1-GFP-X).** Northern blotting and fluorescence microscopy indicate that ORFX was expressed during WIV1 infection. A virus infection assay showed that rWIV1-X replicated as efficiently as rWIV1 in Vero E6, Calu-3, and HeLa-hACE2 cells. Further study showed that ORFX could inhibit interferon production and activate NF- κ B. Our results demonstrate for the first time that the unique ORFX in the WIV1 strain is a functional gene involving modulation of the host immune response but is not essential for in vitro viral replication. Lei-Ping Zeng, a Yu-Tao Gao, Xing-Yi Ge, Qian Zhang, a Cheng Peng, Xing-Lou Yang, a Bing Tan, Jing Chen, Aleksei A. Chmura, **Peter Daszak, Zheng-Li Shi** Key Laboratory of Special Pathogens, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China; **EcoHealth Alliance, New York, New York, USA** https://www.ecohealthalliance.org/wp-content/uploads/2016/11/Zeng-et-al_Bat-SARSLike_2016.pdf

1. Green fluorescent protein (GFP) is a protein in the jellyfish *Aequorea Victoria* that exhibits green fluorescence when exposed to light. The protein has 238 amino acids, three of them (Numbers 65 to 67) form a structure that emits visible green fluorescent light. ... Biologists use GFP as a marker protein. **2017**

EFFICIENT REVERSE GENETIC SYSTEMS FOR RAPID GENETIC MANIPULATION OF EMERGENT AND PREEMERGENT INFECTIOUS CORONAVIRUSES



Adam S Cockrell 1, Anne Beall 2, Boyd Yount 1, Ralph Baric 3 4

Affiliations

1 Department of Epidemiology, University of North Carolina-Chapel Hill, Chapel Hill, NC, USA.

2 Departments of Microbiology and Immunology, University of North Carolina-Chapel Hill, Chapel Hill, NC, USA.

3 Department of Epidemiology, University of North Carolina-Chapel Hill, Chapel Hill, NC, USA.

4 Departments of Microbiology and Immunology, University of North Carolina-Chapel Hill, Chapel Hill, NC, USA. rbaric@email.unc.edu
PMID: 28508214 PMCID: PMC7120940 DOI: 10.1007/978-1-4939-6964-7_5

Abstract "Emergent and preemergent coronaviruses (CoVs) pose a global threat that requires immediate intervention. Rapid intervention necessitates the capacity to generate, grow, and genetically manipulate infectious CoVs in order to rapidly evaluate pathogenic mechanisms, host and tissue permissibility, and candidate antiviral therapeutic efficacy. CoVs encode the largest viral RNA genomes at about 28-32,000 nucleotides in length, and thereby complicate efficient engineering of the genome. **Deconstructing the genome into manageable fragments affords the plasticity necessary to rapidly introduce targeted genetic changes in parallel and assort mutated fragments while maximizing genome stability over time. In this protocol we describe a well-developed reverse genetic platform strategy for CoVs that is comprised of partitioning the viral genome into 5-7 independent DNA fragments (depending on the CoV genome), each subcloned into a plasmid for increased stability and ease of genetic manipulation and amplification.** Coronavirus genomes are conveniently partitioned by introducing type IIS or IIG restriction enzyme recognition sites that confer directional cloning. Since each restriction site leaves a unique overhang between adjoining fragments, reconstruction of the full-length genome can be achieved through a standard DNA ligation comprised of equal molar ratios of each fragment. **Using this method, recombinant CoVs can be rapidly generated and used to investigate host range, gene function, pathogenesis, and candidate therapeutics for emerging and preemergent CoVs both in vitro and in vivo"**

2017 MIT REPORTED

Work at the WIV was indeed progressing quickly. In **2017**, Daszak and Shi followed with another study, also at BSL-2, that one-upped Baric's work in North Carolina. The WIV had continued to unearth dozens of new SARS-like coronaviruses in bat caves, and it reported making chimeras with eight of them by fusing the spikes of the new viruses to the chassis of WIV1. Two of them replicated well in human cells. **They were, for all intents and purposes, brand-new pathogens. The revelation that the WIV was working with SARS-like viruses in subpar safety conditions has led some people to reassess the chance that SARS-CoV-2 could have emerged from some type of laboratory incident.** "That's screwed up," the Columbia University virologist Ian Lipkin, who coauthored the seminal paper arguing that covid must have had a natural origin, told the journalist Donald McNeil Jr. "It shouldn't have happened. People should not be looking at bat viruses in BSL-2 labs. My view has changed." But the WIV was not breaking any rules by working at BSL-2, says Filippa Lentzos, a biosecurity expert at King's College London "There are no enforceable standards of what you should and shouldn't do. It's up to the individual countries, institutions, and scientists." And in China, she says, the vertiginous rise of high-tech biological research has not been accompanied by an equivalent increase in oversight. **In an email, Zhengli Shi said she followed Chinese rules that are similar to those in the US. Safety requirements are based on what virus you are studying. Since bat viruses like WIV1 haven't been confirmed to cause disease in human beings, her biosafety committee recommended BSL-2 for engineering them and testing them and BSL-3 for any animal experiments.** In response to questions about the decision to do the research in BSL-2 conditions, Peter Daszak forwarded a statement from EcoHealth Alliance stating that the organization "must follow the local laws of the countries in which we work" and that the NIH had determined the research was "not gain-of-function."

"Since bat viruses like WIV1 haven't been confirmed to cause disease in human beings, her biosafety committee recommended BSL-2 for engineering them and testing them and BSL-3 for any animal experiments." Shi authored a paper with Baric about bat viruses spilling over into animal than human populations that crowned her The Bat Lady.

JANUARY 2017



A group called Global Virome Project will be visiting Beijing to discuss the scope of the project, which is sponsored by USAID and other organizations. They plan to have US and China be the leaders of the project. The China host is China CDC and our dear friend George Gao is China POC for this project. The purpose of the project is to identify viruses present in the wild life with potential crossing over to humans, causing human infection and disease. Following the identification of the viruses is the development of vaccines to protect human population. China has huge capacity for vaccine development (I think it has 7 national owned vaccine manufacturing facility and over 30 private vaccine making companies). (b) (5) One of the partners in this project is EcoHealth Alliance. **Peter Daszak from EcoHealth Alliance is one of the leaders for the GYP project and he has NIAID grant from ROB looking at the coronaviruses in Bat populations in China in collaboration with Wuhan Institute of Virology. He came to visit me once in the Embassy. This grant has direct connection with the purpose of GVP.** The meeting is scheduled for Feb. 6-7 in Beijing and it is conflict with our Japan EID meeting. Thank you and have a nice weekend. Ping Chen, PhD Director of NIAID Office in China Office of Global Research, NIAID, NIH [Ping Chen, PhD Director of NIAID Office in China Office of Global Research, NIAID, NIH](#)

INSIDE THE CHINESE LAB POISED TO STUDY WORLD'S MOST DANGEROUS PATHOGENS MAXIMUM-SECURITY BIOLAB IS PART OF PLAN TO BUILD NETWORK OF BSL-4 FACILITIES ACROSS CHINA



Virologist Shi Zhengli at the Wuhan Institute of Virology in 2017. Photo: Feature China / Barcroft Studios / Future Publishing / Getty Images

FEBRUARY 22, 2017 The Wuhan Institute of Virology, China's first BIOSAFETY LEVEL-4 LAB (BSL-4), is certified to work on the most dangerous pathogens. Observes *Nature*, "But worries surround the Chinese lab, too. [The SARS virus has escaped from high-level containment facilities in Beijing multiple times.](#)" The Wuhan Institute of Virology is the only BSL-4 virology lab in China staffed with two Chinese virologists, SHI ZHENGLI and Xing-Yi Ge, who both previously worked at a University of North Carolina at Chapel Hill lab, which had already bio-engineered an incredibly virulent strain of bat coronavirus¹.

1. The GoF/GoT experiments were carried out in a BSL-3 and BSL-2 Lab. Other reports say the BSL-4 was postponed until 2018.

In **2017**, she and her colleagues at the Wuhan lab published a paper about an experiment in which they created new hybrid bat coronaviruses by mixing and matching parts of several existing ones — including at least one that was nearly transmissible to humans — in order to study their ability to infect and replicate in human cells.

APRIL 2017



BAT CAVE SOLVES MYSTERY OF DEADLY SARS VIRUS — AND SUGGESTS NEW OUTBREAK COULD OCCUR: CHINESE SCIENTISTS FIND ALL THE GENETIC BUILDING BLOCKS OF SARS IN A SINGLE POPULATION OF HORSESHOE BATS.

NOVEMBER 30, 2017 *Nature Medicine*: "After a detective hunt across China, researchers chasing the origin of the deadly SARS virus have finally found their smoking gun. In a remote cave in Yunnan province, virologists have identified a single population of horseshoe bats that harbours virus strains with all the genetic building blocks of the one that jumped to humans in 2002, killing almost 800 people around the world." And wielding the smoking gun, besides a cast of usual suspects (Xing-Yi Ge and **PETER DASZAK**) was none other than **SHI ZHENGLI** (Zhengli Shi in Chinese), a virologist who is often called China's "bat woman" by her colleagues because of her virus-hunting expeditions in bat caves over the past 16 years. That *Nature Medicine* report was based on an article published in San Francisco-based "PLOS Pathogens" and jointly funded by National Natural Science Foundation of China. <https://www.nature.com/articles/d41586-017-07766-9>

NOVEMBER 2017 DISCOVERY OF A RICH GENE POOL OF BAT SARS-RELATED CORONAVIRUSES PROVIDES NEW INSIGHTS INTO THE ORIGIN OF SARS CORONAVIRUS

Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus

Ben Hu , Lei-Ping Zeng , Xing-Lou Yang , Xing-Yi Ge, Wei Zhang, Bei Li, Jia-Zheng Xie, Xu-Rui Shen, Yun-Zhi Zhang, Ning Wang, Dong-Sheng Luo, Xiao-Shuang Zheng, Mei-Niang Wang, Peter Daszak, Lin-Fa Wang, Jie Cui , Zheng-Li Shi 

[view less]

Published: November 30, 2017 • <https://doi.org/10.1371/journal.ppat.1006698>

"In the current study, we successfully cultured an additional novel SARSr-CoV Rs4874 from a single fecal sample using an optimized protocol and Vero E6 cells. Its S protein shared 99.9% aa sequence identity with that of previously isolated WIV16 and it was identical to WIV16 in RBD. Using the reverse genetics technique we previously developed for WIV1, we constructed a group of infectious bacterial artificial chromosome (BAC) clones with the backbone of WIV1 and variants of S genes from 8 different bat SARSr-CoVs. Only the infectious clones for Rs4231 and Rs7327 led to cytopathic effects in Vero E6 cells after transfection. The other six strains with deletions in the RBD region, Rf4075, Rs4081, Rs4085, Rs4235, As6526 and Rp3 failed to be rescued, as no cytopathic effects was observed and viral replication cannot be detected by immunofluorescence assay in Vero E6 cells. In contrast, when Vero E6 cells were respectively infected with the two successfully rescued chimeric SARSr-CoVs, WIV1-Rs4231S and WIV1-Rs7327S, and the newly isolated Rs4874, efficient virus replication was detected in all infections. **To assess whether the three novel SARSr-CoVs can use human ACE2 as a cellular entry receptor, we conducted virus infectivity studies using HeLa cells with or without the expression of human ACE2. All viruses replicated efficiently in the human ACE2-expressing cells.** The results were further confirmed by quantification of viral RNA using real-time RT-PCR."

<https://journals.plos.org/plospathogens/article?id=10.1371/journal.ppat.1006698>

NOVEMBER 30, 2017 "To assess whether the three novel SARSr-CoVs can use human ACE2 as a cellular entry receptor, we conducted virus infectivity studies using HeLa cells with or without the expression of human ACE2. All viruses replicated efficiently in the human ACE2-expressing cells." Isn't that great. They aimed the virus at human lung tissue that contains ACE2 receptors. This is Gain-of-Function. MIT biologist Kevin Esvelt reviewed a paper that appears to have been published with financial assistance from the Daszak sub-contract grant. According to Esvelt, certain techniques that the researchers used met the definition of Gain-of-Function research.

[GO BACK](#)

TRUMP LIFTS GAIN-OF-FUNCTION / GAIN-OF-THREAT BAN



DECEMBER 19, 2017 The US National Institutes of Health (NIH) announced that they would resume funding Gain-of-Function experiments involving influenza, Middle East respiratory syndrome coronavirus, and **severe acute respiratory syndrome coronavirus**. A moratorium had been in place since October, 2014. At the time, the NIH had stated that the moratorium "will be effective until a robust and broad deliberative process is completed that results in the adoption of a new US Government Gain-of-Function research policy." This process has now concluded. It was spearheaded by the **National Science Advisory Board for Biosecurity (NSABB)** and led to the development of a new framework for assessing funding decisions for research involving pathogens with enhanced pandemic potential. The release of the framework by the Department of Health and Human Services (HHS), of which NIH is part, signalled the end of the funding pause." Francis S. Collins, M.D., Ph.D. Director, National Institutes of Health." It should be noted that the names of the scientists who make these determinations will be TOP SECRET

[https://www.thelancet.com/journals/laninf/article/PIIS1473-3099\(18\)30006-9/fulltext](https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(18)30006-9/fulltext)

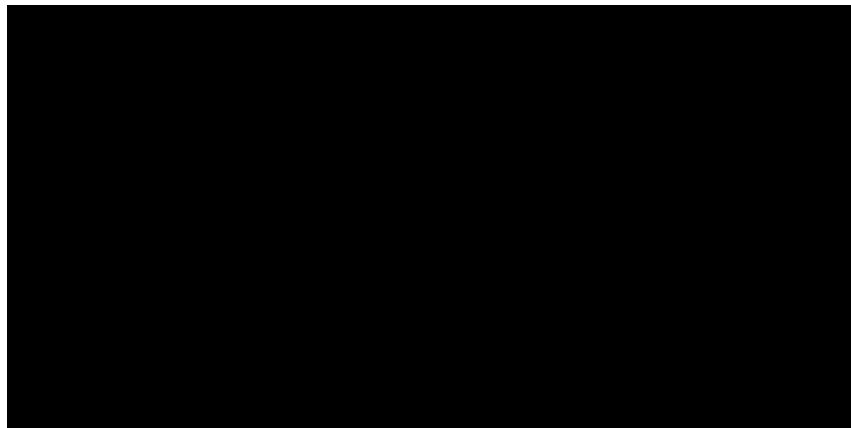
MAY 17, 2017 At a hotel in central Wuhan in May 2017, a former commander at USAMRIID participated in a workshop with the WIV's top scientists. The workshop was called the "Second China-US Workshop on the Challenges of Emerging Infections, Laboratory Safety and Global Health Security. Gain-of-function research, laboratory risks and gene editing were key topics during the conference held from May 17-19. Shi and George F. Gao, the director at the Chinese Centre for Disease Control and Prevention,

gave presentations at the conference hosted by China's Academy of Sciences and attended by the director of Wuhan Institute of Virology BSL-4 laboratory, Yuan Zhiming. (What Really Happened In Wuhan by Sharri Markson 25/5/21)

BSL-4 OPENS AT WIV JANUARY 19, 2018



NIH LIFTS FUNDING PAUSE ON GAIN-OF-THREAT RESEARCH



THE STATE DEPARTMENT CABLES INDICATE A LACK OF TRAINED TECHNICIANS AT WIV



JANUARY 19, 2018 U.S. Embassy in Beijing takes unusual step of repeatedly sending U.S. science diplomats to the Wuhan Institute of Virology. One visit raises so many red flags, that a cable is sent noting, “a serious shortage of appropriately trained technicians and investigators needed to safely operate this high-containment laboratory.” **“During interactions with scientists at the WIV laboratory, they noted the new lab has a serious shortage of appropriately trained technicians and investigators needed to safely operate this high-containment laboratory, the researchers also showed that various SARS-like coronaviruses can interact with ACE2, the human receptor identified for SARS-coronavirus.** This finding strongly suggests that SARS-like coronaviruses from bats can be transmitted to humans to cause SARS-like diseases. From a public health perspective, this makes the continued surveillance of SARS-like coronaviruses in bats and study of the animal-human interface critical to future emerging coronavirus outbreak prediction and prevention.” (JANUARY 19, 2018 , DOS cable, drafted by two officials from the embassy’s environment, science and health sections who met with the WIV scientists.)

JANUARY 2018 Shi was appointed Principal Investigator for a new Strategic Priority Research Program of the Chinese Academy of Sciences (grant no. XBD29010101, \$1.35 million USD), investigating “genetic evolution and transmission mechanism of important bat-borne viruses.” This project, especially with its focus on transmission mechanisms, aligns with the first focus area mentioned above. That same month, Shi began work on a project titled “Study on the evolutionary mechanism of bat SARS-like coronavirus adapted to host receptor molecules and the risk of crossspecies infection.” The project was funded at a value of roughly \$850,000 USD (grant no. 31770175) and is slated to run until December 2021. This grant aligns with the second focus area, the description of which specifically mentions replicating and modifying coronaviruses. [GOP ORIGINS]

BAT CORONAVIRUSES IN CHINA

MARCH 2, 2019 “It is highly likely that future SARS- or MERS-like coronavirus outbreaks will originate from bats, and there is an increased probability that this will occur in China **Shi Zhengli** and her colleagues wrote in a 2019 paper that now seems chillingly prescient. “Therefore, the investigation of bat coronaviruses becomes an urgent issue for the detection of early warning signs.” “Why China? Two bat CoVs caused outbreaks in China; it is thus urgent to study the reasons to avoid future outbreaks. China is the third largest territory and is also the most populous nation in the world. A vast homeland plus diverse climates bring about great biodiversity including that of bats and bat-borne viruses—most of the ICTV coronavirus species were named by Chinese scientists studying local bats or other mammals. The majority of the CoVs can be found in China. Moreover, most of the bat hosts of these CoVs live near humans, potentially transmitting viruses to humans and livestock. Chinese food culture maintains that live slaughtered animals are more nutritious, and this belief may enhance viral transmission. In November 2012, the first case of SARS was recorded in Foshan city, Guangdong Province, China. **In 2005, two independent Chinese groups reported the first bat SARS-related CoV (SARSr-CoV) that was closely related to human SARS-CoV, implying a bat origin of the latter. Since then, more bat SARSr-CoV isolates were identified in China. Genome identities of these bat SARSr-CoVs are as high as 92% to human SARS-CoV, but their major receptor binding spike proteins cannot use the human virus entry receptor ACE2.** Whether they are the progenitor viruses of SARS-CoV is debatable. In 2013, the isolation of a bat SARSr-CoV that uses the ACE2 receptor provided the strongest evidence of the bat origin of SARS-CoV. Furthermore, the building blocks for SARS-CoV were identified from eleven different SARSr-CoV viral strains in a five-year surveillance program in a cave inhabited by multiple species of horseshoe bats in Yunnan Province, China It is generally believed that bat-borne CoVs will re-emerge to cause the next disease outbreak. In this regard, China is a likely hotspot. The challenge is to predict when and where, so that we can try our best to prevent such outbreaks.”
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6466186/>

March 27, 2018 The Wuhan Institute of Virology issues a news release in English after the last of the U.S. Embassy visits. The news release was removed the week of April 6, 2020, although it remains archived on the internet.

APRIL 2018 Have you seen this report? What is the connection between Piglets virus and NIAID? The scientists that helped the farmers identified the virus are from Wuhan Institute of Virology, Dr. Zhengli Shi’s team. Dr. Shi is the Chinese collaborator on a ROB grant award to EcoHealth in NYC. Her lab has published the connection of SARS-like coronavirus found in cave bats in Southwestern China to the SARS that caused human infection in 2003. NIAID funding has supported her research on SARS-like coronaviruses in China. Her team has developed tests to identify SARS-like coronaviruses. The test was used to identify the virus that caused piglets death at the farm. I learned this story last year when she visited embassy with EcoHealth to USAID on the Global Virome Project. Dr. Shi was the researcher who made the arrangement for me to visit WIV’s P41ab. Attached is the research paper and NIAID grant was acknowledged. [JUDICIAL WATCH DOCS](#)





WANG YANYI

WUHAN LAB CHIEF WANG YANYI DISPUTES APRIL 2018 WIV NATURE ARTICLE

APRIL 2018 Wang Yani: "Some of the speculation [of a lab leak] is based on an article the WIV published in *Nature* in April 2018, saying it discovered a novel coronavirus originating from bats. In February 2020, WIV published another article in *Nature* saying another novel coronavirus from bats was discovered, and the similarity between this virus and the Sars-CoV-2 is up to 96.2 per cent. Actually, the virus mentioned in the 2018 article wasn't SARS-CoV-2. The virus in the article mainly causes diarrhoea and death among piglets. It was later named SADS. The genome sequence of SADS is only 50 per cent similar to that of SARS-CoV-2. It's a rather big difference. The bat coronavirus that had a 96.2 per cent genomic similarity to Sars-CoV-2 was **RaTG-13**. From the perspective of many non-professionals, the similarity rate of 96.2 per cent is a very high number. But coronavirus is one of the RNA viruses that have the largest genomes. Take the SARS-CoV-2 for example. Its entire genome contains about 30,000 bases. The difference of a percentage of 3.8 means the difference of over 1,100 nucleotide positions. In the natural world, it takes a long period of time for a virus to naturally evolve and mutate to become Sars-CoV-2. Although the researchers identified the genome sequence of **RaTG-13** they did not isolate nor obtain the live virus of **RaTG-13**. Thus, there is no possibility of us leaking **RaTG-13**." Wang Yani said the institute now had three strains of *live viruses*, including one that was 96 per cent genomically similar to the SARS virus. But their highest similarity to SARS-CoV-2 was only 79.8 per cent." This was a startling admission. if they had viruses 80% similar why not SARS-COV-2?"

<https://www.scmp.com/news/china/science/article/3085825/coronavirus-conspiracy-lab-leak-claims-pure-fabrication-wuhan>

DECEMBER 2019 "I had never expected this kind of thing to happen in Wuhan, in central China," Shi Zhengli told *Scientific American*. "Wuhan is a skyscraper-filled metropolis of 11 million people hundreds of miles from the bat-friendly caves of southern China. Could they have come from our lab?" Shi Zhengli described the next few weeks as the most stressful of her life. She claimed she frantically searched her lab's records, looking for signs of an accident or inappropriate disposal, only relaxing once the genetic code of the new virus was sequenced and didn't match the coronaviruses in her lab. "That really took a load off my mind. I had not slept a wink for days." The Chinese government shows no signs of releasing Shi's lab's records so we have to take her self-serving lies for fact. In any case, while Shi's comments were meant to be reassuring, they actually implied something unsettling. Most of us mistakenly believe that the risk of a biolab-based pandemic is infinitesimal. But clearly Shi Zhengli didn't rule out an accidental escape from her lab. Although we will never get to see her records we do know that Shi Zhengli work at the time involved altering the Spike Protein of Corona viruses found in bats:

Shi Zhengli: "During the past two decades, three zoonotic coronaviruses have been identified as the cause of large-scale disease outbreaks—Severe Acute Respiratory Syndrome (SARS), Middle East Respiratory Syndrome (MERS), and Swine Acute Diarrhea Syndrome (SADS). SARS and MERS emerged in 2003 and 2012, respectively, and caused a worldwide pandemic that claimed thousands of human lives, while SADS struck the swine industry in 2017. They have common characteristics, such as they are all highly pathogenic to humans or livestock, their agents originated from bats, and two of them originated in China. **Thus, it is highly likely that future SARS- or MERS-like coronavirus outbreaks will originate from bats, and there is an increased probability that this will occur in China.** Therefore, the investigation of bat coronaviruses becomes an urgent issue for the detection of early warning signs, which in turn minimizes the impact of such future outbreaks in China. The purpose of the review is to summarize the current knowledge on viral diversity, reservoir hosts, and the geographical distributions of bat coronaviruses in China, and eventually we aim to predict virus hotspots and their cross-species transmission potential."

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6466186>

THE WUHAN INSTITUTE OF VIROLOGY VIRUS DATABASE WAS TAKEN OFFLINE

SEPTEMBER 12, 2019 It has not been published since and has not been made available to World Health Organisation investigators, who did not ask for it during their Wuhan visit earlier this year. Shi has claimed the virus database was taken offline after 3000 hacking attempts. *Vanity Fair* reported "They paid one visit to the Wuhan Institute of Virology, where they met with Shi Zhengli, as recounted in an annex to the mission report. One obvious demand would have been access to the WIV's database of some 22,000 virus samples and sequences, which had been taken offline. At an event convened by a London organization on March 10, 2021 Daszak was asked whether the group had made such a request. He said there was no need: Shi Zhengli had stated that the WIV took down the database due to hacking attempts during the pandemic. "Absolutely reasonable," Daszak said. "And we did not ask to see the data.... As you know, a lot of this work has been conducted with EcoHealth Alliance.... We do basically know what's in those databases. There is no evidence of viruses closer to SARS-CoV-2 than RaTG13 in those databases, simple as that." The GOP ORIGINS REPORT:

<https://www.vanityfair.com/news/2021/06/the-lab-leak-theory-inside-the-fight-to-uncover-covid-19s-origins>

KATIE BO WILLIAMS, CNN INTELLIGENCE AND NATIONAL SECURITY REPORTER: Just a few months before the world becomes aware that there is this dangerous virus circulating in Wuhan, the WIV removes from the internet this catalog of 22,000 viral samples that it had been working on, that it had been studying.

GUPTA (on-camera): What happened to the bat coronavirus database in September of 2019?

DASZAK: They told us they were revising it and making it more searchable and that they would then get hacked over and over again so they didn't put it back up. That's what they told us.

GUPTA: Do you believe that?

DASZAK: Well, it's not my role to believe or not believe. I'm a scientist. I look at data and information and we look at it objectively.

GUPTA: You're a scientist but I'm saying, you know, you do have to look at history as well and there's been concerns that there's been a lack of transparency.

DASZAK: Right. When I look in that database, it was simply a list of samples with sequences attached. Most of which had been published, probably the vast majority by now, so we knew what was in those data bases.

GUPTA: If it was mostly out there.

DASZAK: Yes.

GUPTA: Much of it published, why were they so concerned about it being hacked?

DASZAK: Well, I don't know. I mean, more importantly, people who think that that database has the answers to SARS-COVI-2, I really doubt that.

DATA BASE DISAPPEARS

One of the more informative suppressions of data was the closure of China's main database on bat and other viruses. Zhengli Shi, China's leading expert on bat coronaviruses, told [the BBC](#) that it was taken off line because of numerous hacking attempts. It's conceivable that in January 2020, after the pandemic broke out, people without authorized access might have tried to hack into the database. But in fact the database went off line [on September 12, 2019](#). Who would have wanted to hack into a bat virus database back then? More likely, that is the date at which Chinese authorities realized they had a virus escape problem. [Bulletin of Atomic Scientists](#)

LACK OF CELL PHONE ACTIVITY AT WIV

OCTOBER 2019 A report — obtained by the London-based NBC News Verification Unit — says there was no cellphone activity in a high-security portion of the Wuhan Institute of Virology from October 7, 2019 through October 24, 2019, and that there may have been a "hazardous event" sometime between Oct. 6 2019 and Oct. 11 2019. "Would be interesting if someone analyzed commercial telemetry data at & near Wuhan lab from Oct-Dec 2019," Marco Rubio tweeted. "If it shows dramatic drop off in activity compared to previous 18 months it would be a strong indication of an incident at lab & of when it happened."

<https://www.documentcloud.org/documents/6884792-MACE-E-PAI-COVID-19-ANALYSIS-Redacted.html>

ROAD BLOCKS AROUND WIV

OCTOBER 14-19, 2019 CCP orders roadblocks around WIV.

FINANCING SHI ZHENGLI'S GAIN-OF-FUNCTION / GAIN-OF-THREAT EXPERIMENTS WAS PART OF THE PREDICT PROGRAM AND THAT IS WHY IT WAS SHUT DOWN



OCTOBER 25, 2019 In a move that worries many public health experts, the federal government is quietly shutting down a surveillance program for dangerous animal viruses that someday may infect humans. The United Nations Environment Program estimates that a new animal disease that can also infect humans is discovered every four months. Ending the program, experts fear, will leave the world more vulnerable to lethal pathogens like Ebola and MERS that emerge from unexpected places, such as bat-filled trees, gorilla carcasses and camel barns. The end of the program "is definitely a loss," said Peter Daszak, president of the EcoHealth Alliance, a nonprofit global health organization that received funding from the program. "PREDICT was an approach to heading off pandemics, instead of sitting there waiting for them to emerge and then mobilizing. That's expensive."

<https://www.nytimes.com/2019/10/25/health/predict-usaid-viruses.html>

NOVEMBER 2019 a genetically modified Coronavirus escaped from the Bio Safety Level, BSL-2 lab in Wuhan. These experiments, assuming they should be conducted at all, should have been performed in a BSL-4 lab, but the WIV didn't have one until 2018 and many of these experiments were performed much earlier and their results were stored at the WIV. BSL-4 is for viruses to which there is no known vaccine or therapeutic. Daszak should stand trial in USDC/SDNY. If found guilty he should face the death penalty for mass-murder and treason. Dust off old sparky and execute him. This is personal. I came minutes away from dying of SARS-CoV-19 but came back to life after doctors beat on my chest, then I spent a month in Lenox Hill Hospital in Manhattan with a lung tube in my chest as I had a collapsed lung. The disease left one of my fingers paralyzed. I witnessed the agony and suffering the other patients went through first hand.

NOVEMBER 2019 At least four countries who sent delegations to the MILITARY WORLD GAMES have now confirmed the presence of SARS-CoV-2 or COVID-19 cases within their borders in November and December 2019, before the news of an outbreak first became public.

[GOP ORIGINS REPORT](#)

PATIENTS ZERO

NOVEMBER 2019 The WSJ reported: "Three researchers from China's Wuhan Institute of Virology became sick enough in November 2019 that they sought hospital care, according to a previously undisclosed U.S. intelligence report." While it is not clear what had sickened them they had symptoms similar to SARS-CoV-19, "These were not the janitors," said the former State Department official. "They were active researchers. The dates were among the absolute most arresting part of the picture, because they are smack where they would be if this was the origin." An intelligence analyst working with David Asher sifted through classified channels and turned up a report that outlined why the lab-leak hypothesis was plausible. It had been written in May by researchers at the Lawrence Livermore National Laboratory, which performs national security research for the Department of Energy. But it appeared to have been buried within the classified collections system. "The Wuhan Institute of Virology has not come across such

cases," the Bat Lady wrote to the NYT, "If possible, can you provide the names of the three to help us check?"



WUHAN INSTITUTE OF VIROLOGY CREW

NOVEMBER 18, 2019 The Wuhan Institute of Virology posts a job opening that seeks to fill "1-2 post-doctoral fellows" who will "take bats as the research object and provide answers regarding the molecular mechanism that can co-exist with Ebola and SARS-associated coronaviruses for a long time without causing disease, and its relationship with flight (aerosols) and longevity. Virology, immunology cell biology and multiple omics (refers to biological science study fields that end with -omics) are used to compare the differences between humans and other mammals." Candidates are to send their resumes to Peng Zhou (??) Ph.D., the "**Leader of the Bat Virus Infection and Immunization Group**" at the Wuhan Institute of Virology.

NOVEMBER 21, 2019 Daszak tweeted: "We've made great progress with bat SARS-related CoVs, ID'ing 50 novel strains, sequencing **Spike Protein** genes, ID'ing ones that bind to human cells, using recombinant viruses, humanized mice to see SARS-like signs, and showing some don't respond to MABs, vaccines."



DECEMBER 9, 2019 In a video interview Daszak mentioned the testing of modified coronaviruses on human cells and humanized mice in the WIV, just weeks before the first cases of COVID-19 were announced in the city of Wuhan, China. Daszak has dismissed the possibility of a lab leak, insisting since the start of the pandemic it's a "conspiracy theory" — without providing evidence for his claim. Daszak: "Real conspiracy behind well-funded, politically motivated social media campaigns to create false narrative on COVID origins. Add Falun Gong/Epoch Times, 1000s of 'independent researchers', pseudo-virologists from Fintech¹ /bioinformatics² & right-wing media."

1. Fintech refers to the integration of technology into offerings by financial services companies in order to improve their use and delivery to consumers. It primarily works by unbundling offerings by such firms and creating new markets for them. Startups disrupt incumbents in the finance industry by expanding financial inclusion and using technology to cut down on operational costs.

2. The leading journal in its field, Bioinformatics publishes the highest quality scientific papers and review articles of interest to academic and industrial researchers. Its main focus is on new developments in genome bioinformatics and computational biology...



THIS WEEK IN VIROLOGY

TRANSCRIPTION: "There are dozens and dozens of small spill overs going on on the planet at any one time which we just never see. Sure they never amplify. There are a few cases in there just absorbed in the illness the overall illness of the population right they could say so "who cares?" you know and that's one argument. But our strategy is any one of those could become pandemic there's a lot of stochasticity¹ and what happens then? So if we look at all of them understand patterns try and reduce the number of spillover events we've got you know but if you say these are diverse coronaviruses and you can't vaccinate against them they're no antivirals what do we do? **You're a virologist you know all the stuff; you can manipulate them in the lab pretty easily. It is just Spike Protein that drives a lot of what happens with the anonymous zoonotic risk. So you can get the sequence. You can build the protein and we work with Ralph Baric at University of North Carolina who does this insert into backbone of another virus and do some work in the lab so you can get more predictive.** When you find a sequence you got this diversity. Now the logical progression for vaccines is, if you're going to develop a vaccine for SARS people are going to use. Let's try and insert some of these others and get a better vaccine. If you see something emerging it gives a head start on making a vaccine or a therapeutic.

You know better knowledge of where they are as well so you can put your money into this clinics that matter and that's one of the big things that we've been trying to push. There's a lot of the word PREDICT or the anticipating, forecasting pandemics. **IT DOESN'T MEAN YOU CAN START THEM.** That's the problem there's so... What we're trying to say in a global scale if we can show where the most likely come from the species in most likely's origin and the people most like to get affected a global actor like W.H.O. our national government can better allocate resources to the highest risk. It's very simple so you're doing a lot of activities those are just a few of all the ones you can find."

1. The quality of lacking any predictable order or plan

DASZAK'S EMAIL'S DELETED BETWEEN NOVEMBER 2019 AND JANUARY 2020

Accepted: Updated invitation: ProgCo call @ Mon Dec 2, 2019 1pm - 2pm (EST) (rcolwell@umiacs.umd.edu) Nov 27, 2019 4:24:00 PM EST

Accepted: Updated invitation: ProgCo call @ Mon Dec 2, 2019 1pm - 2pm (EST) (rcolwell@umiacs.umd.edu)

Subject: Accepted: Updated invitation: ProgCo call @ Mon Dec 2, 2019 1pm - 2pm (EST) (rcolwell@umiacs.umd.edu)
From: Rita Colwell <rcolwell@umd.edu>
To: Kevin Olival <olival@ecohealthalliance.org>
Cc: Rita Colwell <rcolwell@g.umd.edu>, Victoria Lord <vlord@g.umd.edu>
Sent: November 27, 2019 4:24:00 PM EST

Declined: Invitation: EcoHealth Alliance Board Dinner @ Thu Jan 9, 2020 6:30pm - 10pm (EST) (rcolwell@umiacs.umd.edu) Jan 8, 2020 9:34:22 AM EST

Declined: Invitation: EcoHealth Alliance Board Dinner @ Thu Jan 9, 2020 6:30pm - 10pm (EST) (rcolwell@umiacs.umd.edu)

Subject: Declined: Invitation: EcoHealth Alliance Board Dinner @ Thu Jan 9, 2020 6:30pm - 10pm (EST) (rcolwell@umiacs.umd.edu)
From: rcolwell@umd.edu
To: hoda@ecohealthalliance.org
Sent: January 8, 2020 9:34:22 AM EST

DECEMBER 2019 - JANUARY 2020 Daszak deleted the e-mails containing his first reaction to the outbreak since he knew very well what had transpired. <https://usrtk.org/biohazards-blog/scientists-masked-involvement-in-lancet-letter-on-covid-origin> GO BACK



DR. FRANCIS S. COLLINS

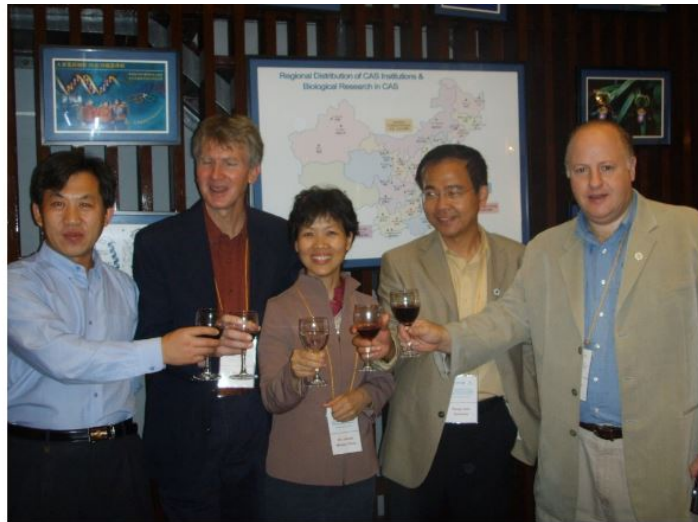
FEDERAL OFFICIALS ENDED A MORATORIUM IMPOSED THREE YEARS AGO ON FUNDING RESEARCH THAT ALTERS GERMS TO MAKE THEM MORE LETHAL

DECEMBER 19, 2019 NYT - "Federal officials ended a moratorium imposed three years ago on funding research that alters germs to make them more lethal. Such work can now proceed, said Dr. Francis S. Collins, the head of the National Institutes of Health, but only if a scientific panel decides that the benefits justify the risks."
<https://www.nytimes.com/2017/12/19/health/lethal-viruses-nih.htm>

EARLY W.H.O. REPORT

JANUARY 5, 2020 "Pneumonia of unknown cause – [China Disease outbreak news January 5, 2020](#). On December 31, 2019, the W.H.O. China Country Office was informed of cases of pneumonia of unknown etiology (unknown cause) detected in Wuhan City, Hubei Province of China. According to the authorities, some patients were operating dealers or vendors in the Huanan Seafood market. **Based on the preliminary information from the Chinese investigation team, no evidence of significant human-to-human transmission and no health care worker infections have been reported.** Based on information provided by national authorities, W.H.O.'s recommendations on public health measures and surveillance of influenza and severe acute respiratory infections still apply. W.H.O. does not recommend any specific measures for travellers. In case of symptoms suggestive of respiratory illness either during or after travel, travellers are encouraged to seek medical attention and share travel history with their healthcare provider. W.H.O. advises against the application of any travel or trade restrictions on China based on the current information available on this event."

<https://www.who.int/csr/don/05-january-2020-pneumonia-of-unknown-cause-china/en/> BARIC: "They created a virus like H5N1 which has a 50 percent mortality rate and they trained it how to be efficiently transmitted in mammals. And so that's scary."



Shi Zhengli (center) and Peter Daszak (far right). (Emerging Viruses Group photo)

DASZAK WORKED CLOSELY WITH ZHENG-LI SHI WHEN SARS-CoV-19 SURFACED

JANUARY 2020 "Zheng-Li Shi, of the Wuhan Institute of Virology, is a senior author of the draft paper (not yet peer reviewed and so far available only in preprint) that gave nCoV-2019 its identity and name. It was Ms. Shi and her collaborators who, back in 2005, showed that the SARS pathogen was a bat virus that had spilled over into people. Ms. Shi and colleagues have been tracing coronaviruses in bats since then, warning that some of them are uniquely suited to cause human pandemics. In a **2017** paper, they set out how, after nearly five years of collecting fecal samples from bats in the Yunnan cave, they had found coronaviruses in multiple individuals of four different species of bats, including one called the intermediate horseshoe bat, because of the half-oval flap of skin protruding like a saucer around its nostrils. The genome of that virus, Ms. Shi and her colleagues have now announced, is 96 percent identical to the Wuhan virus that has recently been found in humans. And those two constitute a pair distinct from all other known coronaviruses, including the one that causes SARS. In this sense, nCoV-2019 is novel — and possibly even more dangerous to humans than the other coronaviruses. I say "possibly" because so far, not only do we not know how dangerous it is, we can't know. Outbreaks of new viral diseases are like the steel balls in a pinball machine: You can slap your flippers at them, rock the machine on its legs and bonk the balls to the jittery rings, but where they end up dropping depends on 11 levels of chance as well as on anything you do. This is true with coronaviruses in particular: They mutate often while they replicate, and can evolve as quickly as a nightmare ghoul. **Peter Daszak, the president of EcoHealth Alliance, a private research organization based in New York that focuses on the connections between human and wildlife health, is one of Ms. Shi's longtime partners. "We've been raising the flag on these viruses for 15 years ever since SARS." He was a co-author of the 2005 bats-and-SARS study, and again of the 2017 paper about the multiple SARS-like coronaviruses in the Yunnan cave. Mr. Daszak told me that, during that second study, the field team took blood samples from a couple of thousand Yunnanese people, about 400 of whom lived near the cave. Roughly 3 percent of them carried antibodies against SARS-related coronaviruses. "We don't know if they got sick. We don't know if they were exposed as children or adults," Mr. Daszak said. "But what it tells you is that these viruses are making the jump, repeatedly, from bats to humans." In other words, this Wuhan emergency is no novel event. It's part of a sequence of related contingencies that stretches back into the past and will stretch forward into the future, as long as current circumstances persist. So when you're done worrying about this outbreak, worry about the next one. Or do something about the current circumstances.**

<https://www.nytimes.com/2020/01/28/opinion/coronavirus-china.html>



ZHENGLI SHI

THE BAT LADY WANTED TO CALL HER VIRUS TARS

"Wuhan Institute of Virology senior scientist Zhengli Shi, who led the re-naming effort, described in an email to University of North Carolina virologist Ralph Baric, "a fierce discussion among Chinese virologists" over the name SARS-CoV-2. Deyin Guo, former dean of Wuhan University's School of Biomedical Sciences and co-author of the name-change proposal, wrote to CSG members that they had failed to consult their naming decision with "virologists including the first discoverers [sic] of the virus and the first describers of the disease" from mainland China. "It is not appropriate to use one disease-based virus' name (like SARS-CoV) to name all other natural viruses that belong to the same species but have very different properties," he wrote in the correspondence sent on behalf of himself and five other Chinese scientists. The group proposed an alternative name – "Transmissible acute respiratory coronavirus (TARS-CoV). Another option, they said, could be "Human acute respiratory coronavirus (HARS-CoV)."

JANUARY 24, 2020 Analysis published in the *Lancet*: "From JANUARY 10, 2020, we enrolled a family of six patients who travelled to Wuhan from Shenzhen between Dec 29, 2019 and Jan 4, 2020. Of six family members who travelled to Wuhan, five were identified as infected with the novel coronavirus. Additionally, one family member, who did not travel to Wuhan, became infected with the virus after several days of contact with four of the family members. None of the family members had contacts with Wuhan markets or animals, although two had visited a Wuhan hospital. Five family members (aged 36–66 years) presented with fever, upper or lower respiratory tract symptoms, or diarrhoea, or a combination of these 3–6 days after exposure. They presented to our hospital (The University of Hong Kong-Shenzhen Hospital, Shenzhen) 6–10 days after symptom onset. They and one asymptomatic child (aged 10 years) had radiological ground-glass lung opacities."

New England Journal of Medicine <https://www.nejm.org/doi/full/10.1056/NEJMoa2001316>

RECTIFICATION OF LAB THAT MAPPED GENOME

JANUARY 2020 The Shanghai laboratory where researchers published the world's first genome sequence of the deadly coronavirus that causes Covid-19 has been shut down. The laboratory at the Shanghai Public Health Clinical Centre was ordered to close for "rectification" on January 12, 2020 a day after Professor Zhang Yongzhen's team published the genome sequence on open platforms. It closed temporarily the following day.

WIV WAS CALLING IN OUTSIDERS TO HELP WITH BIOSAFETY

JANUARY 2020 Relying on the major science and technology infrastructure, this project aims to cultivate national high-level biosafety talents, to output significant scientific and technological breakthroughs and achievements, and to promote the scientific and technological support capabilities for biosafety and public health. According to the scientific and technological development programs of China, Chinese Academy of Sciences (CAS) and Wuhan Institute of Virology (WIV), CAS, the Call Announcement 2020 of Advanced Customer Cultivation Project of Wuhan National Biosafety Laboratory, CAS is released. Please apply for the project accordingly. The specific contents are as below...The research achievements attained during the project implementation, including theses, monographs, patents, software and database etc. shall be marked with "Funded by Advanced Customer Cultivation Project of Wuhan National Biosafety Laboratory, Chinese Academy of Sciences". Any achievements unmarked will not be counted in the assessment. Wuhan Institute of Virology Chinese Academy of Sciences Jan 15th, 2020

http://english.whiov.cas.cn/Notice2016/202001/t20200115_229449.html



National Health Commission of the People's Republic of China
中华人民共和国国家卫生健康委员会

JANUARY 3, 2020 Wuhan Institute of Virology's director general, **Dr. WANG YANYI**, messaged her colleagues, saying the National Health Commission told her the lab's SARS-CoV-2 data shall not be published on social media and shall not be disclosed to the media. And on JANUARY 3, 2020 the commission sent this document, never posted online, but saved by researchers, **telling labs to destroy SARS-CoV-2 samples or send them to the depository institutions designated by the state**. Late Friday [May 16, 2020] the Chinese government admitted to the destruction ... but said it was for public safety. The Chinese government explanation for the destruction of SARS-CoV-2 samples has no scientific credibility. For purposes of "public safety" any samples would surely be stored and studied, exactly as with the ones that were isolated from patients, and their RNA genomes decoded and published. (PBS News Hour May 22, 2020)

The National Health Commission is dictated to by the Leading Party Members' Groups. "Article 46 A leading Party members' group may be formed in the leading body of a central or local state organ, people's organization, economic or cultural institution or other non-Party unit. The group plays the role of the core of leadership. Its main tasks are: to see to it that the Party's line, principles and policies are implemented, to discuss and decide on matters of major importance in its unit, to do well in managing affairs concerning cadres, to unite with the non-Party cadres and the masses in fulfilling the tasks assigned by the Party and the state and to guide the work of the Party organization of the unit and those directly under it."

FEBRUARY 2020 When the lab's Shi Zhengli and colleagues published a paper with the virus's partial genome, they omitted any mention of the special sequence that supercharges the virus or the rare double CGG section. Yet the fingerprint is easily identified in the data that accompanied the paper. Was it omitted in the hope that nobody would notice this evidence of the gain-of-function origin? But in a matter of weeks virologists Bruno Coutard and colleagues published their discovery of the sequence in CoV-2 and its novel supercharged site. Double CGG is there; you only have to look. They comment in their paper that the protein that held it "may provide a gain-of-function" capability to the virus, "for efficient spreading" to humans. [Wall Street Journal Opinion](#)

DASZAK CLAIMS HE WARNED THE WORLD ABOUT COVID

FEBRUARY 27, 2020 In early 2018, during a meeting at the World Health Organization in Geneva, a group of experts I belong to (R&D Blueprint) coined the term "Disease X" We were referring to the next pandemic, which would be caused by an unknown, novel pathogen that hadn't yet entered the human population. As the world stands today on the edge of the pandemic precipice, it's worth taking a moment to consider whether Covid-19 is the disease our group was warning about. Disease X, we said back then, would likely result from a virus originating in animals and would emerge somewhere on the planet where economic development drives people and wildlife together. Disease X would probably be confused with other diseases early in the outbreak and would spread quickly and silently; exploiting networks of human travel and trade, it would reach multiple countries and thwart containment. Disease X would have a mortality rate higher than a seasonal flu

but would spread as easily as the flu. It would shake financial markets even before it achieved pandemic status. In a nutshell, Covid-19 is Disease X. Even as there are signs that **the epidemic's spread might be slowing in China**, multiple communities and countries have now reported sustained transmission in their midst. The number of confirmed cases **has exploded in South Korea** in recent days. In Italy, villages and towns are on lockdown, **Fashion Week in Milan has been disrupted** and festivals are being canceled while public health authorities search for patient zero to identify who else is likely infected and may spread the disease in Europe. Iran appears to have become **a new hub of transmission**. The looming pandemic will challenge us in new ways, as people try to evade quarantines, and **misinformation campaigns and conspiracy theorists ply their trade in open democracies**. But as the world struggles to respond to Covid-19, we risk missing the really big picture: Pandemics are on the rise, and we need to contain the process that drives them, not just the individual diseases. Plagues are not only part of our culture; they are caused by it. **The Black Death** spread into Europe in the mid-14th century with the growth of trade **along the Silk Road**. New strains of influenza have emerged from livestock farming. **Ebola, SARS, MERS** and now **Covid-19** have been linked to wildlife. Pandemics usually begin as viruses in animals that jump to people when we make contact with them.

These spillovers are increasing exponentially as our ecological footprint brings us closer to wildlife in remote areas and the wildlife trade brings these animals into urban centers. Unprecedented road-building, deforestation, land clearing and agricultural development, as well as globalized travel and trade, make us supremely susceptible to pathogens like coronaviruses.

Yet the world's strategy for dealing with pandemics is woefully inadequate. Across the board, from politicians to the public, we treat pandemics as a disaster-response issue: We wait for them to happen and hope a vaccine or drug can be developed quickly in their aftermath. But even as Covid-19 rages, there still is no vaccine available for the SARS virus of 2002-3, nor for HIV/AIDS or Zika or a host of emerging pathogens. The problem is that between outbreaks, the will to spend money on prevention wanes, and the market for vaccines and drugs against sporadic viral diseases isn't enough to drive research and development. During its World Health Assembly in 2016, the W.H.O. set up the R&D Blueprint to bridge this gap and announced a priority list of pathogens that most threaten global health and for which no vaccines or drugs were in the pipeline. SARS made the list, as did MERS, Nipah, Ebola and other rare but serious diseases caused by epidemic viruses. The **Coalition for Epidemic Preparedness Innovations** — a global partnership between public, private, philanthropic and civil society organizations launched at Davos in 2017 — stepped up to the plate and sourced funding to develop vaccines and therapeutics against some of these. To escape from the Age of Pandemics, we'll need to treat them as a public health issue and start working on prevention in addition to responses. Our first goal should be to broaden our armory against potential mass epidemics. When some of us **added "Disease X" to the W.H.O.'s priority list** two years ago, we wanted to make the point that it's not sufficient to develop vaccines and drugs for known agents when the next big one is likely to be a different pathogen — a virus close to SARS, say, but not close enough that the same vaccine can work against both. As Covid-19 strikes today and a spate of other pathogens are ready to emerge in the future, we continue to butt up against nature. Scientists estimate that there are 1.67 million unknown viruses of the type that have previously emerged in people. Discovering and sequencing them should be a priority — a simple case of "know your enemy." In the aftermath of SARS, research on coronaviruses originating in bats has discovered more than 50 related viruses, some of which have the potential to infect people; this information can now be used to test for broad-action vaccines and drugs. Scaling up this effort to cover all viral families, as the **Global Virome Project** proposes to do, is a logical first step toward prevention.

A radical shift is also needed in the way that tests, vaccines and drugs are designed so that entire groups of pathogens are targeted instead of individual pathogens that are already known. The National Institute of Allergy and Infectious Diseases in the United States is working on a **universal flu vaccine** that would cover all known strains of influenza; a universal coronavirus vaccine, an Ebola-virus vaccine and others will also be needed.

With a smaller investment, we can also try to get ahead of pandemics by working with communities in hot spots of emerging diseases. Disease surveillance should be focused on farmers, rural communities and anyone who has extensive contact with wildlife, to look for unusual illnesses, test for novel pathogens and work with people to develop alternatives to high-risk activities such as the wildlife trade.

Pandemics are like terrorist attacks: We know roughly where they originate and what's responsible for them, but we don't know exactly when the next one will happen. They need to be handled the same way — by identifying all possible sources and dismantling those before the next pandemic strikes.

Peter Daszak is a disease ecologist and the president of EcoHealth Alliance, in New York.

<https://www.nytimes.com/2020/02/27/opinion/coronavirus-pandemics.html>

KRISTIAN ANDERSON EARLY EMAIL

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 1 Feb 2020 18:43:31 +0000
To: Kristian G. Andersen
Subject: RE: FW: Science: Mining coronavirus genomes for clues to the outbreak's origins

Thanks, Kristian. Talk soon on the call.

From: Kristian G. Andersen (b) (6) >
Sent: Friday, January 31, 2020 10:32 PM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Cc: Jeremy Farrar (b) (6) >
Subject: Re: FW: Science: Mining coronavirus genomes for clues to the outbreak's origins

Hi Tony,

Thanks for sharing. Yes, I saw this earlier today and both Eddie and myself are actually quoted in it. It's a great article, but the problem is that our phylogenetic analyses aren't able to answer whether the sequences are unusual at individual residues, except if they are completely off. On a phylogenetic tree the virus looks totally normal and the close clustering with bats suggest that bats serve as the reservoir. The unusual features of the virus make up a really small part of the genome (<0.1%) so one has to look really closely at all the sequences to see that some of the features (potentially) look engineered.

We have a good team lined up to look very critically at this, so we should know much more at the end of the weekend. I should mention that after discussions earlier today, Eddie, Bob, Mike, and myself all find the genome inconsistent with expectations from evolutionary theory. But we have to look at this much more closely and there are still further analyses to be done, so those opinions could still change.

Best,
Kristian

On Fri, Jan 31, 2020 at 18:47 Fauci, Anthony (NIH/NIAID) [E] (b) (6) wrote:

FEBRUARY 3, 2020 Thanks for sharing. Yes, I saw this earlier today and both Eddie and myself are actually quoted in it. It's a great article, but the problem is that our phylogenetic analyses aren't able to answer whether the sequences are unusual at individual residues, except if they are completely off. On a phylogenetic tree the virus looks totally normal and the close clustering with bats suggest that bats serve as the reservoir. **The unusual features of the virus make up a really small part of the genome (<0.1%) so one has to look really closely at all the sequences to see that some of the features (potentially) look engineered..** We have a good team lined up to look very critically at this, so we should know much more at the end of the weekend. **I should mention that after discussions earlier today, Eddie, Bob, Mike, and myself all find the genome inconsistent with expectations from evolutionary theory.** But we have to look at this much more closely and there are still further analyses to be done, so those opinions could still change.

When Anderson realized that the NIH and Fauci were involved he said that his was preliminary research because his employer, The Scripps Institute, received most of its funding from the NIH and you don't bite the hand that feeds you.

<https://www.causeiq.com/organizations/scripps-research-institute.330435954>

On **FEBRUARY 19, 2020**, The Lancet, among the most respected and influential medical journals in the world, published a statement that roundly rejected the lab-leak hypothesis, effectively casting it as a xenophobic cousin to climate change denialism and anti-vaxxism. Signed by 27 scientists, the statement expressed "solidarity with all scientists and health professionals in China" and asserted: "We stand together to strongly condemn conspiracy theories suggesting that COVID-19 does not have a natural origin."



KRISTIAN ANDERSON

"Yet there have been no preprints or official scientific reports on the sampling, so it's not clear which, if any, animals tested positive. "Until you consistently isolate the virus out of a single species, it's really, really difficult to try and determine what the natural host is," says Kristian Andersen, an evolutionary biologist at Scripps Research.

KRISTIAN ANDERSON

While the analyses above suggest that SARS-COV-2 may bind human ACE2 with high affinity, computational analyses predict that the interaction is not ideal so it could not be man-made otherwise the binding would be ideal? Doesn't that depend on skill of the scientist or scientists altering the virus? **GO BACK**

IT'S NOT FROM THE LAB BECAUSE KRISTIAN ANDERSON COULD HAVE DESIGNED A BETTER VIRUS

FRANCIS 'THE TALKING MULE' COLLINS: "We debated up one side down the other, and ultimately decided if you were a human trying to design a really dangerous coronavirus, you would not design this one."

The study carefully examined whether key elements of the virus, particularly the spike protein on its surface, appeared engineered. They did not. **The spike didn't optimally bind to its receptor, ACE-2, and the interaction between the two proteins was unpredictable even using the most advanced computer algorithms.** Another key feature often cited as evidence of laboratory origin is the furin cleavage site, where the spike protein is cut in half to "activate" viral material for entry into cells. The viruses most closely related to SARS-CoV-2 don't have this site, but many others do, including other human coronaviruses. The furin site of SARS-CoV-2 has odd features that no human would design. Its sequence is suboptimal, meaning its cleavage by the enzyme furin is relatively inefficient. Any skilled virologist hoping to give a virus new properties this way would insert a furin site known to be more efficient. The SARS-CoV-2 site has more of the hallmarks of sloppy natural evolution than a human hand. Indeed, a timely analysis last year showed convincingly that it is a product of genetic recombination, a natural feature of coronavirus replication and evolution.

WAO

The virus was not man made because it is likely that SARS-COV-2-LIKE VIRUSES with partial or full POLYBASIC CLEAVAGE SITE PRRA will be discovered in other species It has yet to be discovered.

Insertion of a FURIN CLEAVAGE SITE at the S1-S2 JUNCTION enhances cell-cell fusion without affecting viral entry is false.

SARS-CoV-2 could have been derived from a new virus backbone

Anderson's bias against trump affects his research. Tweet deleted

ZHENG-LI SHI: A PNEUMONIA OUTBREAK ASSOCIATED WITH A NEW CORONAVIRUS OF PROBABLE BAT ORIGIN

FEBRUARY 3, 2020 Since the outbreak of severe acute respiratory syndrome (SARS) 18 years ago, a large number of SARS-related coronaviruses (SARSr-CoVs) have been discovered in their natural reservoir host, bats. Previous studies have shown that some bat SARSr-CoVs have the potential to infect humans. Here we report the identification and characterization of a new coronavirus (2019-nCoV), which caused an epidemic of acute respiratory syndrome in humans in Wuhan, China. **The epidemic, which started on December 12, 2019, had caused 2,794 laboratory-confirmed infections including 80 deaths by January 26, 2020.** Full-length genome sequences were obtained from five patients at an early stage of the outbreak. **The sequences are almost identical and share 79.6% sequence identity to SARS-CoV. Furthermore, we show that 2019-nCoV is 96% identical at the whole-genome level to a bat coronavirus.** Pairwise protein sequence analysis of seven conserved non-structural proteins domains show that this virus belongs to the species of SARSr-CoV. In addition, 2019-nCoV virus isolated from the bronchoalveolar lavage fluid of a critically ill patient could be neutralized by sera from several patients. **Notably, we confirmed that 2019-nCoV uses the same cell entry receptor—Angiotensin Converting Enzyme II (ACE2)—as SARS-CoV.** Characterization of full-length genome sequences from patients infected with a new coronavirus (2019-nCoV) shows that the sequences are nearly identical and indicates that the virus is related to a bat coronavirus."

<https://www.nature.com/articles/s41586-020-2012-7>*

This is true. 2019-nCoV is related as a Coronavirus found in Horseshoe Bats because a natural SARS-CoV virus was modified by inducing mutations and a monster virus was created.

NEW BIOSECURITY LAW DECREED IN CHINA

On **FEBRUARY 14, 2020** to the surprise of NSC officials, President Xi Jinping of China announced a plan to fast-track a new biosecurity law to tighten safety procedures throughout the country's laboratories.

KRISTIAN ANDERSON STATEMENT IN SUPPORT OF THE SCIENTISTS, PUBLIC HEALTH PROFESSIONALS, AND MEDICAL PROFESSIONALS OF CHINA COMBATting COVID-19

FEBRUARY 2020 The rapid, open, and transparent sharing of data on this outbreak is now being threatened by rumours and misinformation around its origins. We stand together to strongly condemn conspiracy theories suggesting that COVID-19 does not have a natural origin. Scientists from multiple countries have published and analysed genomes of the causative agent, severe acute respiratory syndrome coronavirus (SARS-CoV-2), and they overwhelmingly conclude that this coronavirus originated in wildlife, as have so many other emerging pathogens. This is further supported by a letter from the presidents of the US National Academies of Science, Engineering, and Medicine and by the scientific communities they represent. Conspiracy theories do nothing but create fear, rumours, and prejudice that jeopardise our global collaboration in the fight against this virus. We support the call from the Director-General of WHO to promote scientific evidence and unity over misinformation and conjecture. We want you, the science and health professionals of China, to know that we stand with you in your fight against this virus.

[https://www.thelancet.com/journals/lancet/article/PIIS0140-6736\(20\)30418-9/fulltext](https://www.thelancet.com/journals/lancet/article/PIIS0140-6736(20)30418-9/fulltext)

MARCH 17, 2020 Nick Wade: "A statement which had enormous influence in shaping public attitudes was a letter (in other words an opinion piece, not a scientific article) published on March 17, 2020 in the journal *Nature Medicine*. Its authors were a group of virologists led by Kristian G. Andersen of the Scripps Research Institute. "Our analyses clearly show that SARS-CoV-2 is not a laboratory construct or a purposefully manipulated virus," the five virologists declared in the second paragraph of their letter. True, some older methods of cutting and pasting viral genomes retain tell-tale signs of manipulation. But newer methods, called "no-see-um" or "seamless" approaches, leave no defining marks. Nor do other methods for manipulating viruses such as serial passage, the repeated transfer of viruses from one culture of cells to another. If a virus has been manipulated, whether with a seamless method or by serial passage, there is no way of knowing that this is the case. Dr. Andersen and his colleagues were assuring their readers of something they could not know."

MARCH 2020 "Despite extensive contact tracing of early cases during the COVID-19 pandemic, there have been no reported cases related to any laboratory staff at the WIV and all staff in the laboratory of Dr. Shi Zhengli were reported to be seronegative for SARS-CoV-2 when tested in March 2020 10.

CHINESE ATTEMPT TO PROVE THAT THE UNIQUE CORONA VIRUS WAS FOUND IN NATURE

MARCH 2020 "ABSTRACT: The SARS-CoV-2 epidemic started in late December 2019 in Wuhan, China, and has since impacted a large portion of China and raised major global concern. Herein, we investigated the extent of molecular divergence between SARS-CoV-2 and other related coronaviruses. Although we found only 4% variability in genomic nucleotides between SARS-CoV-2 and a bat SARS-related coronavirus (SARSr-CoV; RaTG13), the difference at neutral sites was 17%, suggesting **the divergence between the two viruses is much larger than previously estimated. Our results suggest that the development of new variations in functional sites in the receptor-binding domain (RBD) of the spike seen in SARS-CoV-2 and viruses from pangolin SARSr-CoVs are likely caused by natural selection besides recombination.** Population genetic analyses of 103 SARS-CoV-2 genomes indicated that these viruses had two major lineages (designated L and S), that are well defined by two different SNPs¹ that show nearly complete linkage across the viral strains sequenced to date. We found that L lineage was more prevalent than the S lineage within the limited patient samples we examined. **The implication of these evolutionary changes on disease etiology remains unclear.** These findings strongly underscore the urgent need for further comprehensive studies that combine viral genomic data, with epidemiological studies of coronavirus disease 2019 (COVID-19)." It is an a priori assumption that these anomalies were natural.

<https://academic.oup.com/nsr/article/7/6/1012/5775463>

1. To make new cells, an existing cell divides in two. But first it copies its DNA so the new cells will each have a complete set of genetic instructions. Cells sometimes make mistakes during the copying process - kind of like typos. These typos lead to variations in the DNA sequence at particular locations, called single nucleotide polymorphisms, or SNPs (pronounced "snips").

OXFORD UNIVERSITY PUBLICATION NATURE "ENGINEERED BAT VIRUS STIRS DEBATE OVER RISKY RESEARCH: LAB-MADE CORONA VIRUS RELATED TO SARS CAN INFECT HUMAN CELLS"

MARCH 2020 Retraction of earlier article: "Oxford University publication *Nature* "Engineered bat virus stirs debate over risky research: lab-made corona virus related to SARS can infect human cells" "Editors' note, We are aware that this story is being used as the basis for unverified theories that the novel coronavirus causing COVID-19 was engineered. There is no evidence that this is true; scientists believe that an animal is the most likely source of the coronavirus. In the version of this article initially published online, the authors omitted to acknowledge a funding source, USAID-EPT-PREDICT funding from EcoHealth Alliance, to Z.-L.S. [Shi Zhengli] The error has been corrected for the print, PDF and HTML versions of this article." *Nature* is subservient to China so they had to issue this retraction.

<https://www.insidehighered.com/news/2018/10/03/book-publishers-part-ways-springer-nature-over-concerns-about-censorship-china>

THE CHINESE RESEARCHERS AT WIV WERE RECEIVING ASSISTANCE FROM THE GALVESTON NATIONAL LABORATORY AT THE UNIVERSITY OF TEXAS MEDICAL BRANCH AND OTHER U.S. ORGANIZATIONS, BUT THE CHINESE REQUESTED ADDITIONAL HELP

APRIL 14, 2020 "The cables argued that the United States should give the Wuhan lab further support, mainly because its research on bat coronaviruses was important but also dangerous." [washingtonpost.com/opinions/2020/04/14/state-department-cables-warned-safety-issues-wuhan-lab-studying-bat-coronaviruses/](https://www.washingtonpost.com/opinions/2020/04/14/state-department-cables-warned-safety-issues-wuhan-lab-studying-bat-coronaviruses/) In 2020 WIV tried to recruit a new staff <http://english.whiov.cas.cn> GO BACK

WHY CITE EXEMPTION FIVE?

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Fri, 17 Apr 2020 02:45:01 +0000
To: Collins, Francis (NIH/OD) [E]
Subject: RE: [conspiracy](#) gains momentum

Francis:
[REDACTED] (b) (5)
Best,
Tony

From: Collins, Francis (NIH/OD) [E] [REDACTED] (b) (6)
Sent: Thursday, April 16, 2020 5:02 PM
To: Fauci, Anthony (NIH/NIAID) [E] [REDACTED] (b) (6)
Cc: Tabak, Lawrence (NIH/OD) [E] [REDACTED] (b) (6); Lane, Cliff (NIH/NIAID) [E]
[REDACTED] (b) (6); Burklow, John (NIH/OD) [E] [REDACTED] (b) (6)
Subject: conspiracy gains momentum

[REDACTED] (b) (5)
[REDACTED]
<https://www.mediaite.com/tv/foxs-bret-baier-sources-increasingly-confident-coronavirus-outbreak-started-in-wuhan-lab/>

[REDACTED] (b) (5)
Francis

APRIL 17, 2020 Exemption 5 is commonly interpreted as shielding from release draft government documents, records of sensitive deliberations before decisions are made, and government attorney-client deliberations. These types of documents deserve some protection. But agencies stretch the exemption to inappropriately cover other information, such as records that may paint the agency in a bad light, records that reveal problems, and records that contain embarrassing information.

TRUMP CUTS OFF FUNDS TO ECOHEALTH ALLIANCE

APRIL 28, 2020 "A grant to a New York nonprofit ECOHEALTH ALLIANCE aimed at detecting and preventing future outbreaks of coronaviruses from bats has been canceled by the National Institutes of Health, Politico reports, apparently at the direction of President Donald Trump because the research involved the Wuhan Institute of Virology in China. On April 14, 2020 *The Washington Post* published a column highlighting State Department cables about concerns regarding safety at the institute." <https://www.the-scientist.com/news-opinion/nih-cancels-funding-for-bat-coronavirus-research-project-7486>

Dr. Shi Zhengli: "I have conducted collaborative research with Dr. Peter Daszak, President and PI of EcoHealth Alliance. We have established a good relationship in the fields of virus surveillance and pathogen discovery. Our research team has found a variety of coronaviruses with different sequences in bat populations. [Her researchers also created new viruses"]. Some of them have the potential to spread to humans and animals, such as SARS-related coronavirus, MERS-related coronavirus, SADS-related coronavirus, etc. The findings provide important clues for the prevention and control of infectious diseases. We don't understand the NIH termination of funding support for our collaborative project and feel it is absolutely absurd."

APRIL 2020 Daszak: "What worries me the most is that we are going to miss the next emerging disease, that moves from one part of the planet to another, wiping out people as it moves along." Daszak said the purpose of his non-profit was "to develop tools that could help researchers create diagnostics, treatments and vaccines for human outbreaks." <https://www.sciencemag.org/news/2020/04/nih-s-axing-bat-coronavirus-grant-horrible-precedent-and-might-break-rules-critics-say>

THE UNITED STATES DEPARTMENT OF EDUCATION HAS ASKED THE UNIVERSITY OF TEXAS NATIONAL SCIENCE ADVISORY BOARD FOR BIOSECURITY (NSABB) TO PROVIDE DOCUMENTATION OF ITS DEALINGS WITH THE WIV

MAY 1, 2020 "U.S. officials are investigating the Wuhan Institute of Virology as a potential source of the coronavirus pandemic. The request for records of gifts or contracts from the Wuhan Institute of Virology and its researcher Dr. Shi Zhengli known for her work on bats, is of a broader department investigation into possible faulty financial disclosures of foreign money by the Texas group of universities. As one of the nation's 14 Bio Safety Level 4 laboratories, the Galveston National Laboratory at UTMB belongs to the

National Institute of Allergy and Infectious Diseases (NIAID) Biodefense Laboratory Network. It has collaborated with more than 70 countries and with scientists from the U.S. and abroad on biosafety and biosecurity, as part of its broad mission to advance global scientific collaboration. While it receives no financial support or gifts from global scientific laboratories, UTMB complies with obligations to report fiduciary relationships as required by statute."

<https://www.wsj.com/articles/u-s-probes-university-of-texas-links-to-chinese-lab-scrutinized-over-coronavirus-11588325401>

National Science Advisory Board for Biosecurity (NSABB)

James W. LeDuc, PhD

Director, Galveston National Laboratory

Professor, Department of Microbiology and

Immunology

University of Texas Medical Branch

<https://osp.od.nih.gov/biotechnology/national-science-advisory-board-for-biosecurity-nsabb/> (DEAD LINK)

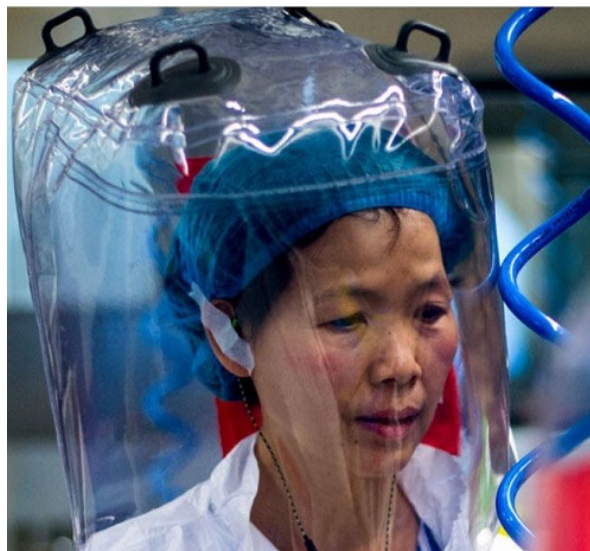
WEIFENG SHI CLAIMS ANOMALOUS INSERTIONS CAN HAPPEN NATURALLY



WEIFENG SHI RmYN02

MAY 10, 2020 In the journal *Current Biology*, researchers describe a recently identified bat coronavirus that is SARS-CoV-2's closest relative in **some regions of the genome and which contains insertions of amino acids at the junction of the S1 and S2 subunits of the virus's Spike Protein in a manner similar to SARS-CoV-2.** While it's not a direct evolutionary precursor of SARS-CoV-2, this new virus, RmYN02, suggests that these types of seemingly unusual insertion events can occur naturally in coronavirus evolution, the researchers say. "Since the discovery of SARS-CoV-2 there have been a number of unfounded suggestions that the virus has a laboratory origin," says senior author Weifeng Shi, director and professor at the Institute of Pathogen Biology at Shandong First Medical University in China. "In particular, it has been proposed the **S1/S2** insertion is highly unusual and perhaps indicative of laboratory manipulation. Our paper shows very clearly that these events occur naturally in wildlife. This provides strong evidence against SARS-CoV-2 being a laboratory escape."

<https://www.technologynetworks.com/genomics/news/spotlight-on-coronavirus-evolution-as-sars-cov-2-relative-is-found-in-bats-334649>



ZHENGLI SHI

TWO WUHAN INSTITUTE OF VIROLOGY SCIENTISTS, XING-YI GE AND ZHENGLI-LI SHI, USE REVERSE GENETICS TO GENERATE A CHIMERICAL VIRUS CLOSELY RESEMBLING THE NOVEL CORONAVIRUS COVID-19

MAY 13, 2020: Two Wuhan Institute of Virology scientists, Xing-Yi Ge and **Zhengli-Li Shi**, use reverse genetics to generate a chimeric virus (one that has been created by combining cells of more than one distinct genotype) **closely resembling the novel coronavirus Covid-19:** “On the basis of these findings, we synthetically re-derived an infectious full-length SHC014 recombinant virus and demonstrate robust viral replication both in vitro and in vivo.” The *Nature Medicine* article also mentions, “Human lungs for HAE cultures were procured under University of North Carolina at Chapel Hill Institutional Review Board–approved protocols.” The Chinese government’s poor record of transparency; the fact that the Wuhan Institute of Virology, a research center with facilities in the same city where the virus first appeared, was studying and creating new dangerous pathogens, including bat coronaviruses cannot be easily dismissed.

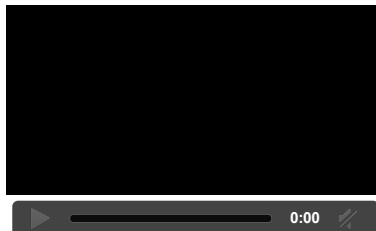
ORIGIN AND CROSS-SPECIES TRANSMISSION OF BAT CORONAVIRUSES IN CHINA

MAY 2020 Alice Latinne, Ben Hu, Kevin J. Olival, Guangjian Zhu, Libiao Zhang, Hongying Li, Aleksei A. Chmura, Hume E. Field, Carlos Zambrana-Torrel, Jonathan H. Epstein, Bei Li, Wei Zhang, Lin-Fa Wang, **Zheng-Li Shi**, **Peter Daszak** This article is a preprint and has not been certified by peer review. Importantly, the closest known relative of SARS-CoV-2, a SARS-related virus, was found in a *Rhinolophus* sp. bat in this region, although it is important to note that our survey was limited to China, and that the bat hosts of this virus also occur in nearby Myanmar and Lao PDR. The article really says nothing new. [DOI: https://doi.org/10.1101/2020.05.31.116061](https://doi.org/10.1101/2020.05.31.116061)

MAY 2020 “It was the ‘incompetence of China,’ and nothing else, that did this mass world-wide killing,” Trump tweeted.

MAY 2020 Anthony Fauci tells *National Geographic* that “everything about the stepwise evolution over time strongly indicates that [this virus] evolved in nature and then jumped species.”

POMPEO SAYS VIRUS WAS FROM LAB THEN WALKS IT BACK



MIKE POMPEO

MAY 16, 2020 “Sadly, we’re not much further than we were weeks and weeks ago,” Pompeo said when asked how the investigation is going. “The Chinese Communist Party has relentlessly deceived and denied information to the west. We have repeatedly asked to have teams go in and assist them to identify where the virus originated. We know it began in Wuhan, but we don’t know from where or from whom, and those are important things. Your listeners need to know. We still need to know that so we can break the code on this thing. One of the key facts for scientists and epidemiologists to build out vaccines and therapeutics and to identify how this was ultimately delivered to the world. You have to know where patient zero began and how patient zero became infected. Yet, the Chinese Communist Party has at every turn attempted to manage the World Health Organization to manage the information flow, to punish doctors who wanted to talk about this publicly, to undermine the central understandings of transparency that every country has a responsibility to deliver. As a result of that, we still have so many unanswered questions. We, the United States, the world, have so many unanswered questions that are incredibly important so we can address these issues going forward to keep the American people safe. This isn’t political. This isn’t aimed at achieving a political victory. It’s aimed squarely at getting the right health outcomes and saving lives across the world.”

<https://www.breitbart.com/politics/2020/05/16/exclusive-secretary-pompeo-president-trump-committed-to-holding-chinese-communist-party-accountable-for-coronavirus-pandemic>

TRUMP WANTED AN INVESTIGATION OF THE ORIGIN OF THE VIRUS

MAY 19, 2020 “In early January, for example, China ordered samples of the virus to be destroyed, depriving the world of critical information. Even now, China continues to undermine the International Health Regulations by refusing to share accurate and timely data, viral samples and isolates, and by withholding vital information about the virus and its origins. And, to this day, China continues to deny international access to their scientists and relevant facilities, all while casting blame widely and recklessly and censoring its own experts...The World Health Organization has failed to publicly call on China to allow for an independent investigation into the origins of the virus, despite the recent endorsement for doing so by its own Emergency Committee. The World Health Organization’s failure to do so has prompted World Health Organization member states to adopt the “COVID-19 Response” Resolution at this year’s World Health Assembly, which echoes the call by the United States and so many others for an impartial, independent, and comprehensive review of how the World Health Organization handled the crisis. **The resolution also calls for an investigation into the origins of the virus, which is necessary for the world to understand how best to counter the disease.**”

<https://web.archive.org/web/20200601041112/https://www.whitehouse.gov/wp-content/uploads/2020/05/Tedros-Letter.pdf>

TRUMP ENDS GRANT TO ECHO HEALTH ALLIANCE

MAY 21, 2020 Days after the news conference in April, the National Institutes of Health emailed Peter Daszak, the head of EcoHealth Alliance. They questioned his work with the Wuhan Institute, and after an exchange of emails, he was informed that the renewal of his grant for more than \$3 million was canceled.

<https://www.nytimes.com/2020/05/21/health/wuhan-coronavirus-laboratory.html>

ECO-HEALTH ALLIANCE GET ANONYMOUS GRANT FROM A CCP PUPPET



May 27, 2020 at 8:13 PM Randy W Schekman¹ wrote: "Dear Peter, I am part of the Rich Roberts group and helped to line-up more Laureates to join the petition to Azar and Collins. We don't expect a response from them but we wish to make a constructive contribution to your essential work and have resolved to help find private funds to offset your loss. **Our first success is with a foundation that makes anonymous contributions to various causes including in support of biomedical science.** I am pleased to report that this group will provide the EcoHealth Alliance a grant of \$500,000 to at least partially offset the NIH funds that were withdrawn from your program. Since they wish to remain anonymous, I will be happy to serve as the intermediary in transfer of funds to your program. We can communicate about how to proceed. Best wishes, Randy Schekman HHMI Investigator Dept. of Mol. and Cell Biology Li Ka Shing² Center UC Berkeley Berkeley, CA 94720-3370 (510) 642-5686 Stephanie Canon Assistant to Randy Schekman 484 Li Ka Shing Center Berkeley, CA 94720-3370 (510) 642-0594 stephaniecanon@berkeley.edu Re: A contribution to your work May 27, 2020 9:04:00 PM EDT Aleksei Chmura

1. Randy W. Schekman The Nobel Prize in Physiology or Medicine 2013 Prize motivation: "for their discoveries of machinery regulating vesicle traffic, a major transport system in our cells."

2. Li Ka Shing is considered to be a top pro-Beijing figure. Also in 2005, Li donated US\$40 million to the University of California, Berkeley, citing that he was impressed with the university's accomplishments in the biosciences. In recognition of Li's donation, the university has named the campus' new biosciences facility the Li Ka Shing Center for Biomedical and Health Sciences, which opened in October 2011 https://en.wikipedia.org/wiki/Li_Ka-shing One of Li Ka Shing's Hutchison Optel Telecom Technology Co., Ltd.; had ties to the Chinese Military.

<https://www.commerce.gov/news/press-releases/2020/12/commerce-department-will-publish-first-milkoopitary-end-user-list-naming-companies-connected-to-Chinese-Military>



SHI ZHENG LI

MAY 28, 2020 After the breakout Shi Zheng Li disappeared then made an appearance on TV to show she was alive and not liquidated by the CCP.

TRUMP PULLS USA OUT OF W.H.O.

MAY 29, 2020 TRUMP: "The Chinese government has continually violated its promises to us and so many other nations these plain facts cannot be overlooked or swept aside. The world is now suffering as a result of the malfeasance of the Chinese government. China's cover-up of the Wuhan virus allowed the disease to spread all over the world instigating a global pandemic that has cost more than 100,000 in American lives and over a million lives worldwide. Chinese officials ignored their reporting obligations to the World Health Organization and pressured the World Health Organization to mislead the world when the virus was first discovered by Chinese authorities. Countless lives have been taken and profound economic hardship has been inflicted all around the globe. They strongly recommended against me doing the early ban from China but I did it anyway it was proven to be 100% correct. China has total control over the World Health Organization despite only paying 40 million dollars per year compared to what the United States

has been paying which is approximately 450 million dollars a year. We have detailed the reforms that it must make and engage with them directly but they have refused to act because they have failed to make the requested and greatly needed reforms. We will be today terminating our relationship with the World Health Organization and redirecting those funds to other worldwide and serving urgent global public health needs. The world needs answers from China on the virus. We must have transparency. Why is it that China shut off infected people from Wuhan to all other parts of China. It went nowhere else. It didn't go to Beijing it went nowhere else but they allowed them to freely travel throughout the world including Europe and the United States. The death and destruction caused by this is incalculable. We must have answers not only for us but for the rest of the world. This pandemic has underscored the crucial importance of building up America's economic independence reshoring our critical supply chains and protecting America's scientific and technological advances. For years the government of China has conducted illicit espionage to steal our industrial secrets of which there are many today I will issue a proclamation to better secure our nation's vital university research and to suspend the entry of certain foreign nationals from China who we have identified as potential security risks." <https://www.rev.com/blog/transcripts/donald-trump-press-conference-transcript-on-china-hong-kong-and-the-who>

NIH GRANT REINSTATED BUT THE MONEY CAN'T BE SUB-AWARDED TO THE WIV

JULY 2020 Drs. Aleksei Chmura and Peter Daszak EcoHealth Alliance, Inc. 460 W 34th St Suite 1701 New York, NY 10001 Re: NIH Grant R01AI110964 Dear Drs. Chmura and Daszak:

"In follow-up to my previous letter of April 24, 2020, I am writing to notify you that the National Institute of Allergy and Infectious Diseases (NIAID), an Institute within the National Institutes of Health (NIH), under the Department of Health and Human Services (HHS), has withdrawn its termination of grant R01AI110964, which supports the project Understanding the Risk of Bat Coronavirus Emergence. Accordingly, the grant is reinstated. However, as you are aware, the NIH has received reports that the Wuhan Institute of Virology (WIV), a subrecipient of EcoHealth Alliance under R01AI110964, has been conducting research at its facilities in China that pose serious bio-safety concerns and, as a result, create health and welfare threats to the public in China and other countries, including the United States."

Grant award R01AI110964 is subject to biosafety requirements set forth in the NIH Grants Policy Statement (e.g., NIH GPS, Section 4.1.24 "Public Health Security") and the Notice of Award (e.g., requiring that "Research funded under this grant must adhere to the [CDC/NIH Biosafety in Microbiological and Biomedical Laboratories (BMBL)]."). Moreover, NIH grant recipients are expected to provide safe working conditions for their employees and foster work environments conducive to high-quality research. NIH GPS, Section 4. The terms and conditions of the grant award flow down to subawards to subrecipients. 45 C.F.R. § 75.101. *As the grantee, EcoHealth Alliance was required to "monitor the activities of the subrecipient as necessary to ensure that the subaward is used for authorized purposes, in compliance with Federal statutes, regulations, and the terms and conditions of the subaward . . ."* 45 C.F.R. § 75.352(d). *We have concerns that WIV has not satisfied safety requirements under the award, and that EcoHealth Alliance has not satisfied its obligations to monitor the activities of its subrecipient to ensure compliance. Moreover, as we have informed you through prior Notices of Award, this award is subject to the Transparency Act subaward and executive compensation reporting requirement of 2 C.F.R. Part 170. To date you have not reported any subawards in the Federal Subaward Reporting system.*

Therefore, effective the date of this letter, July 8, 2020, NIH is suspending all activities related to R01AI110964, until such time as these concerns have been addressed to NIH's satisfaction. This suspension is taken in accordance with 45 C.F.R. § 75.371, Remedies for Noncompliance, which permits suspension of award activities in cases of non-compliance, and the NIH GPS, Section 8.5.2, which permits NIH to take immediate action to suspend a grant when necessary to protect the public health and welfare. This action is not appealable in accordance with 42 C.F.R. § 50.404 and the NIH GPS Section 8.7, Grant Appeals Procedures. However, EcoHealth Alliance has the opportunity to provide information and documentation demonstrating that WIV and EcoHealth Alliance have satisfied the above-mentioned requirements. Specifically, to address the NIH's concerns, EcoHealth must provide the NIH with the following information and materials, which must be complete and accurate:

1. Provide an aliquot¹ of the actual SARS-CoV-2 virus that WIV used to determine the viral sequence.
2. **Explain the apparent disappearance of Huang Yanling, a scientist / technician who worked in the WIV lab but whose lab web presence has been deleted.**
3. Provide the NIH with WIV's responses to the 2018 U.S. Department of State cables regarding safety concerns.
4. **Disclose and explain out-of-ordinary restrictions on laboratory facilities, as suggested, for example, by diminished cell-phone traffic in October 2019, and the evidence that there may have been roadblocks surrounding the facility from October 14-19, 2019.**
5. Explain why WIV failed to note that the RaTG13 virus, the bat-derived coronavirus in its collection with the greatest similarity to SARS-CoV-2, was actually isolated from an abandoned mine where three men died in 2012 with an illness remarkably similar to COVID-19, and explain why this was not followed up.
6. Additionally, EcoHealth Alliance must arrange for WIV to submit to an outside inspection team charged to review the lab facilities and lab records, with specific attention to addressing the question of whether WIV staff had SARS-CoV-2 in their possession prior to December 2019. The inspection team should be granted full access to review the processes and safety of procedures of all of the WIV field work (including but not limited to collection of animals and biospecimens in caves, abandoned man-made underground cavities, or outdoor sites). The inspection team could be organized by NIAID, or, if preferred, by the U.S. National Academy of Sciences.
7. Lastly, EcoHealth Alliance must ensure that all of its subawards are fully reported in the Federal Subaward Reporting System. During this period of suspension, NIH will continue to review the activities under this award, taking into consideration information provided by EcoHealth Alliance, to further assess compliance by EcoHealth Alliance and WIV, including compliance with other terms and conditions of award that may be implicated. Additionally, during the period of suspension, EcoHealth Alliance may not allow research under this project to be conducted. Further, no funds from grant R01AI110964 may be provided to or expended by EcoHealth Alliance or any subrecipients; all such charges are unallowable. It is EcoHealth Alliance's responsibility as the recipient of this grant award to ensure that the terms of this suspension are communicated to and understood by all subrecipients. EcoHealth Alliance must provide adequate oversight to ensure compliance with the terms of the suspension. Any noncompliance of the terms of this suspension must be immediately reported to NIH. Once the original award is reinstated, NIH will take additional steps to restrict all funding in the HHS Payment Management System in the amount of \$369,819. EcoHealth Alliance will receive a revised Notice of Award from NIAID indicating the suspension of these research activities and funding restrictions as a specific condition of award. Please note that this action does not preclude NIH from taking additional corrective or enforcement actions pursuant to 45

CFR Part 75, including, but not limited to, terminating the grant award. NIH may also take other remedies that may be legally available if NIH discovers other violations of terms and conditions of award on the part of EcoHealth Alliance or WIV. Sincerely, Michael S Lauer, MD NIH Deputy Director for Extramural Research. http://downloads.vanityfair.com/lab-leak-theory/Daszak_7_8_20_Reactivation_and_Suspension.pdf

1. A portion of a larger whole, especially a sample taken for chemical analysis or other treatment.



DR. PETER DASZAK

HEADLINES READ: HEINOUS! CORONA VIRUS RESEARCHER SHUT DOWN FOR WUHAN-LAB LINK SLAMS NEW FUNDING RESTRICTIONS
PETER DASZAK, PRESIDENT OF THE RESEARCH ORGANIZATION ECOHEALTH ALLIANCE, DESCRIBES HOW HE HAS BEEN CAUGHT IN
POLITICAL CROSS-HAIRS OVER HIS PARTNERSHIP WITH A VIROLOGY LAB IN CHINA.

AUGUST 2020 The US National Institutes of Health (NIH) has reinstated a research organization's multimillion-dollar grant to study how coronaviruses move from bats to people — which it cancelled in a controversial move earlier this year. But as Peter Daszak, the head of the **small non-profit organization — EcoHealth Alliance in New York City — found out in early July, the funding can't be used unless the organization meets what he says are absurd conditions.** The demands, detailed in a letter from the NIH, are politically motivated, he says. **To carry out its research, EcoHealth Alliance partners with the Wuhan Institute of Virology (WIV) in China, which has been at the centre of unfounded rumours that the COVID-19 pandemic was caused by a coronavirus released from its laboratory.** The NIH cancelled EcoHealth Alliance's grant in April 2020, days after US President Donald Trump told a reporter that the United States would stop funding work at the WIV. EcoHealth Alliance and Daszak have been working with Shi Zhengli, a virologist at the WIV, for more than 15 years. Since 2014, an NIH grant has funded EcoHealth's research in China, which involves collecting faeces and other samples from bats, and blood samples from people at risk of infection from bat-origin viruses. Scientific studies suggest that the SARS-CoV-2 coronavirus most likely originated in bats, and research on the topic could be crucial to identifying other viruses that might cause future pandemics. **The WIV is a subrecipient on the grant.** The NIH makes seven demands of EcoHealth; these were first reported by the Wall Street Journal this week, and have been viewed by Nature. The agency asks EcoHealth to obtain a vial of the SARS-CoV-2 sample that was used by the WIV to determine the virus's genetic sequence. It also requests that EcoHealth arrange an inspection of the WIV by US federal officials. Daszak calls the demands from the NIH "heinous", and worries that the funding freeze is delaying vital work to identify and prevent the next pandemic. The NIH declined to comment, saying that the agency does not disclose internal deliberations on a specific grant. In an e-mail to Nature, Shi calls the NIH's demands "outrageous" and echoes Daszak's assertions that the agency's demands are unrelated to the WIV's collaboration with EcoHealth. Nature spoke with Daszak about being caught in the political cross-hairs.

How have you been doing since your grant was suspended?

DASZAK: It's just a very difficult and disappointing and worrisome time. I've lost people that I know to COVID-19. It's a bat-origin coronavirus. We should have been there trying to find out why this thing emerged. And right now I'm sat in my house, looking out the window, unable to do this work, because the NIH has told us that it's not appropriate. It's extremely frustrating.

What is the aim of the project that's been affected?

DASZAK: We have specific aims: to go into rural regions of China to find bat-origin coronaviruses and determine which ones are high risk, then to work with local communities in rural China in five provinces. We target communities that are at high risk for viral 'spillover' and see whether they're getting infected — and then finally see whether people are getting sick from novel coronaviruses.

How have you responded to the NIH's letter?

DASZAK: We've written to the NIH and said: we think that this is inappropriate and wrong for the following reasons. Please, allow us to continue this work. But I doubt they're going to do that right now. The NIH have told us not to work on this project. Obviously, we're not going to break any NIH rules. **But we have an ongoing collaboration, we have data that we've gathered over 15 years of working in China — 5 years under a previous grant from the NIH — which haven't been published yet.** So we need to carry on with that work.

How is your work relevant to the pandemic today?

DASZAK: We estimate that every single day, somebody in China or in southeast Asia gets infected with a new bat coronavirus. Right now, somebody is walking around, and they might be developing the first signs of a cough from the next COVID. We fully intend to be an organization that helps to prevent the next pandemic. That is our mission.

The NIH has asked you to obtain a vial of isolated SARS-CoV-2 from the WIV. Did you work on the novel coronavirus during your project?

DASZAK: The grant isn't used to fund work on SARS-CoV-2. Our organization has not actually published any data on SARS-CoV-2.

We work on bat coronaviruses that are out there in the wild and try to predict what the next one is. We don't work on sequencing SARS-CoV-2. It's absurd because it's absolutely outside the remit of the work we do.

Your grant has received widespread attention in the past few months. How has that been?

DASZAK: Conspiracy-theory outlets and politically motivated organizations have made Freedom of Information Act requests on our grants and all of our letters and e-mails to the NIH. We don't think it's fair that we should have to reveal everything we do. When you submit a grant, you put in all your best ideas. **We don't want to hand those over to conspiracy theorists for them to publish and ruin and make a mockery of.**

What are you most worried about?

DASZAK: We're not a political organization. We're just trying to do good work to prevent pandemics. We're feeling the pressure of a very aggressive administration in the US picking fights with a country where we happen to be collaborating. And it turns out that they decided that this issue and our work is going to be one of the angles of attack. That's extremely unfortunate. The winner in all of this is the virus, and not just this virus — SARS-CoV-2 — but all the other viruses.

8/21/2020 <https://www.nature.com/articles/d41586-020-02473-4>

The GOP ORIGINS REPORT: "In an August 21, 2020, interview with Nature, after the NIH suspended the grants he was using to fund research at the WIV, Daszak claimed "The grant isn't used to fund work on SARS-CoV-2. Our organization has not actually published any data on SARSCoV-2." This is despite the fact that four days later Nature Communications published "Origin and cross-species transmission of bat coronaviruses in China." Daszak, Shi, Hu, and Wang are all listed as authors, with Shi and Daszak both being listed as corresponding authors. The preprint for the article was uploaded on May 31, 2020, almost three months before Daszak's interview with Nature. The paper includes a phylogenetic analysis "suggesting a likely origin for SARS-CoV-2 in Rhinolophus spp. bats." Daszak, Shi, three EcoHealth Alliance affiliated researchers, and Linfa Wang are credited with designing the study, conducting fieldwork, and establishing collection and testing protocols.

AUGUST 2020 EcoHealth Alliance Inc Grantee Website New York, New York, United States Purpose To support India's Ministry of Animal Husbandry and Dairying for establishment of National One Health Platform **AUGUST 2020** REGION SERVED GLOBAL, ASIA COMMITTED AMOUNT \$1,499,414 GRANT TOPIC Agricultural Development DURATION (MONTHS) 37 GRANTEE LOCATION New York, New York, United States

TRUMP WANTS TO FORM A COMMISSION TO LOOK INTO THE WIV LAB LEAK

AUGUST 2020 The draft executive order created the "Trump Commission" named Sen. Tom Cotton as the commissioner, while Pompeo's senior policy adviser Mary Kissel and his China adviser Miles Yu were to act as co-chair and vice co-chair or executive director. Retired Air Force Brig. Gen. Robert Spalding would lead the sessions on the geo-politics, and a general from Fort Detrick, the US biological weapons defense program in Maryland, would run the virology portion of the inquiry to investigate whether the virus had been manipulated in a lab. In a highly controversial move, Trump's top adviser on the coronavirus, Fauci, would be hauled in to explain why he funded risky coronavirus research in China and the not-for-profit EcoHealth Alliance president Peter Daszak would be grilled on the missing virus database from the Wuhan Institute of Virology, among other topics, such as why he outsourced this dangerous research to China.

EXECUTIVE ORDER

NATIONAL COMMISSION ON THE ORIGINS AND COSTS OF COVID-19

By the authority vested in me as President by the Constitution and the laws of the United States of America, it is hereby ordered as follows:

Section 1. Establishment. The National Commission on the Origins and Costs of COVID-19 ("Commission") is hereby established.

Sec. 2. Membership. (a) The Commission shall be chaired by Senator Thomas B. Cotton and consist of the following members:

- (i) at least three scientists with expertise in virology or infectious diseases;
 - (ii) at least two economists with expertise in estimating the macroeconomic costs of exogenous shocks such as COVID-19, including the costs associated with loss of life;
 - (iii) one or more individuals with expertise in the geopolitics or military strategy of the People's Republic of China; and
 - (iv) one or more individuals from any other area determined by the President to be relevant to the Commission in fulfilling its duties.
- (b) The Chair shall designate from among the Commission members one member to serve as Vice-Chair.

Sec. 3. Mission and Purpose. (a) The Commission shall investigate the origins of the COVID-19 pandemic; the economic, political, social, human, and other costs of the pandemic borne by the United States; and whether the People's Republic of China or the Chinese Communist Party have used the pandemic to advance their own economic, geopolitical, military, or territorial agendas. In conducting its investigation, the Commission shall:

- (i) create a comprehensive timeline of events of the COVID-19 pandemic;
- (ii) document the facts and circumstances surrounding the origins of the COVID-19 pandemic and any efforts to hide its origins;
- (iii) identify actions of governments, actors, organizations, and other entities that may have played a material role in concealing the dangers presented by COVID-19, including human-to-human transmission of the virus;
- (iv) estimate the economic costs to the United States traceable to COVID-19, accounting for, among other things, any reduction in economic output, productivity, wages, and real estate values; any price gouging and hoarding; and the expenditure of significant government funds to fight the effects of the pandemic;
- (v) estimate the human costs to the United States traceable to COVID-19, including loss

of life directly from the virus and indirectly from factors such as pandemic-related delays in delivering health screenings or medical treatments and the emotional distress associated with tragic and disruptive events such as the loss of loved ones and the shutdown of critical institutions such as schools, childcare centers, workplaces, and houses of worship; and

(vi) identify actions taken by the People's Republic of China or the Chinese Communist Party, or any other organization, individual, or entity acting in cooperation with the People's Republic of China or Chinese Communist Party, to use the pandemic to advance economic, geopolitical, military, or territorial agendas.

(b) The Commission shall recommend actions that the Federal Government may take to recover any damages as well as all costs estimated under sections 3(a)(iv) and (v) of this order from any entities identified during the investigation required by section 3(a)(iii) of this order.

Sec. 4. Administration. (a) The Commission shall have a staff, headed by an Executive Director. The Executive Director shall be appointed by the Chair. In the event of a vacancy, a new Executive Director shall be appointed or designated by the Chair.

(b) The Department of State shall provide administrative support and funding for the Commission, to the extent permitted by law.

(c) The heads of all executive departments and agencies, to the extent permitted by law and consistent with their ongoing responses to COVID-19, shall provide the Commission such information and cooperation as it may require for purposes of carrying out its mission.

(d) The Commission shall, as necessary, hold public hearings and shall request information, including relevant documents, from Federal, State, and local officials, nongovernmental organizations, private entities, scientific institutions, industry and workforce representatives, and others affected by COVID-19.

(e) The Commission shall consult with distinguished individuals from outside the Federal Government, who shall not provide their individualized advice to the Commission. These individuals shall include:

(e) The Commission shall consult with distinguished individuals from outside the Federal Government, who shall not provide their individualized advice to the Commission. These individuals shall include:

(i) scientists with expertise in virology or infectious diseases;

(ii) economists with expertise in estimating the economic costs of exogenous shocks, including the costs associated with loss of life and emotional distress within communities; and

(iii) experts on the geopolitical or military strategies, and the economic and territorial objectives, of the People's Republic of China and the Chinese Communist Party.

(f) On a periodic basis, but not less than once every 30 days, the Commission shall provide a detailed update to the Attorney General on the status and scope of its investigation, with an emphasis on any developments that might affect ongoing or anticipated civil or criminal enforcement activities by the Department of Justice.

(g) The Commission shall meet as required by the Chair; and, unless extended by the President, shall terminate within 60 days of accomplishing the objectives set forth in this order and delivering its final report as specified in subsection (h) of this section.

(h) The Commission shall submit to the President through the Chair:

(i) an interim report within 45 days of the date of this order; and

(ii) a final report for public release within 120 days of the date of this order.

(i) scientists with expertise in virology or infectious diseases;

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- (ii) a final report for public release within 120 days of the date of this order.

JANUARY 2021

FEBRUARY 2021 Biden orders Pompeo investigation of WIV shut down writing it off as Trump conspiracy theory. Daszak: "Questions were raised about the legitimacy of the findings and the project was deemed to be an ineffective use of resources, explained a source familiar with the decision."

CHAPTER 24

CHI COM AGENT OF INFLUENCE DASZAK HEADED W.H.O. TEAM THAT SUGGESTED COVID-19 ORIGINATED IN BARCELONA - ENTERED CHINA VIA FROZEN MEAT



PETER COTTINGTON DASZAK

THE BARCELONA BEEF THEORY W.H.O. LEGITIMATIZED

THE WALL STREET JOURNAL: HOW THE W.H.O.'S HUNT FOR COVID'S ORIGINS STUMBLED IN CHINA

MARCH 29, 2021 "One member of the team of experts, Peter Daszak, a British disease ecologist who runs EcoHealth Alliance, a New York-based pandemic prevention group, pushed back against the criticism of the team's work and of China's level of cooperation. He said the lab leak hypothesis was "political from the start." Dr. Daszak added that the W.H.O. team was not restricted in its interviews with scientists who were on the ground at the start of the pandemic. He himself has been accused of having a conflict of interest because of his past research on coronaviruses with the Wuhan Institute of Virology, which, he said, was what a disease ecologist should be doing. "We were in the right place because we knew that there was a risk of the virus emerging," said Dr. Daszak. "We were working there with this exact viral group and it happened." <https://www.nytimes.com/2021/03/29/world/asia/china-virus-WHO-report.htm>

"It included one scientist from the U.S.: Peter Daszak, a zoologist and president of EcoHealth Alliance, a New York-based nonprofit. Dr. Daszak had experience hunting for the origins of emerging human viruses in animals, including 16 years working with researchers in China. He was on a team that pinpointed bats as the source of the coronavirus behind SARS. Some U.S. officials and scientists were concerned some of his nonprofit's work in China posed a conflict of interest. EcoHealth had in past years provided funding to the Wuhan Institute of Virology as part of a grant from the U.S. National Institutes of Health. The WIV is at the center of assertions by the Trump administration that the pandemic virus could have come from a lab, and Dr. Daszak had publicly dismissed the possibility. In applying for a spot on the team, Dr. Daszak said, he described his expertise and provided a conflict-of-interest statement to the W.H.O. including his work with the WIV. "I'm known to W.H.O., and I'm known for my work on this," he told the Journal. "I recognized the historical importance of it and the value I would be able to bring to it." The W.H.O.'s Mr. Jasarevic said Dr. Daszak's expertise in studying bats and zoonotic diseases was "good experience for the team" and didn't pose a conflict of interest. Dr. Daszak said he asked WIV researchers on the visit why a database of viruses the institute had publicly posted had been taken offline. Dr. Shi responded that the institute had had to take down the database—an Excel spreadsheet—after about 3,000 hacking attempts, Dr. Daszak said. The decision to rank the lab theory as "extremely unlikely" was unanimous, they said. "I waited until everyone else had passed their opinion and then I passed mine," Dr. Daszak said, "because of the sensitivities around my work with the Wuhan lab." [READ THE WALL STREET JOURNAL ARTICLE IN FULL](#)

ACCORDING TO W.H.O.'S REPORT DASZAK'S JOINT INTERNATIONAL TEAM EXAMINED FOUR SCENARIOS:

- Direct zoonotic transmission to humans (spillover);
- Introduction through an intermediate host followed by spillover;
- Introduction through the (cold) food chain;
- Introduction through a laboratory incident.

For each of these possible pathways of emergence, the joint team conducted a qualitative risk assessment, considering the available scientific evidence and findings. It also stated the arguments against each possibility. The team assessed the relative likelihood of these pathways and prioritized further studies that would potentially increase knowledge and understanding globally. The joint team's assessment of likelihood of each possible pathway was as follows:

- Direct zoonotic spillover is considered to be a possible-to-likely pathway;
- Introduction through an intermediate host is considered to be a likely to very likely pathway; the possible intermediate host of sars-cov-2 remains elusive.

- Introduction through cold/ food chain products is considered a possible pathway;
- **Introduction through a laboratory incident was considered to be an extremely unlikely pathway.**



DASZAK IN COMMUNIST CHINA

THE W.H.O. TEAM PUSHES THE PREPOSTEROUS THEORY THAT THE VIRUS WAS SPREAD TO HUMANS IN SHIPMENTS OF FROZEN FOODS FROM SPAIN

"The W.H.O. team opened the door to a theory embraced by Chinese officials, saying it was possible the virus might have spread to humans through shipments of frozen food, an idea that has gained little traction with scientists outside China. And the experts pledged to investigate reports that the virus might have been present outside China months before the outbreak in Wuhan in late 2019, a longstanding demand of Chinese officials. The virus was circulating in Wuhan several weeks before it appeared at the Hunan Seafood Wholesale Market, where some of the earliest clusters were initially reported, the experts said. Chinese officials heavily promoted the idea that the virus came from abroad at the news conference on Tuesday, **arguing that the search for the origin of the virus should focus on places outside China.**"

<https://www.forbesindia.com/article/global-news/china-scores-a-public-relations-win-after-who-mission-to-wuhan/66349/1>

<https://www.nytimes.com/2021/02/09/world/asia/wuhan-china-who-covid.html>



"A team of experts selected by the World Health Organization to investigate the origins of the virus that caused the Covid-19 pandemic returned last week from Wuhan, site of the world's first outbreak. The team, having broken the ice with Chinese scientists, plans to produce a joint report on the possible origins of the virus. The two groups of scientists, from China and the W.H.O., agreed to pursue some ideas that the Chinese government has been promoting, like the possibility that the virus was transported on frozen food. But the W.H.O. team also became frustrated by China's refusal to turn over raw data for analysis. Peter Daszak, a member of the W.H.O. team and the president of EcoHealth Alliance in New York, is primarily concerned with the animal origins of the virus. A specialist in animal diseases and their spread to humans, Dr. Daszak has worked with the Wuhan Virology Institute, a collaboration that last year prompted the Trump administration to cancel a grant to his organization. In an interview after his return to New York, he said that the visit had provided some new clues, which all of the scientists, Chinese and international, agreed most likely pointed to an animal origin within China or Southeast Asia. The scientists have largely discounted claims that the virus originated in a lab, saying that possibility was so unlikely that it was not worth further investigation." <https://www.nytimes.com/2021/02/14/health/WHO-covid-daszak-china-virus.html>



"The supply chains to Huanan market included cold-chain products and animal products from 20 countries, including those where samples have been reported as positive for SARS-CoV-2 before the end of 2019 and those where close relatives of SARS-CoV-2 are found. There is evidence that some domesticated wildlife the products of which were sold in the market

are susceptible to SARS-CoV, but none of the animal products sampled in the market tested positive in this study. *In the early phase of pandemic, due to lack of awareness of the potential role of cold chain in virus introduction and transmission, the cold-chain products were not tested. These findings, however, do raise the possibility of different potential pathways of introduction. Preliminary sampling and testing of other markets in Wuhan and upstream suppliers to the Huanan market taken during 2020 did not reveal evidence of SARS-CoV-2 circulating in animals. SARS-CoV-2 has been found to persist in conditions found in frozen food, packaging and cold-chain products. Index cases in recent outbreaks in China have been linked to the cold chain; the virus has been found on packages and products from other countries that supply China with cold-chain products, indicating that it can be carried long distances on cold-chain products. Further analysis will examine spatial and temporal correlations and correct for underlying biases in sampling, and also to trace frozen products back to the Huanan market from suppliers"*

The Spanish flu, also known as the 1918 influenza pandemic, was an unusually deadly influenza pandemic caused by the H1N1 influenza A virus. Lasting from February 1918 to April 1920, it infected 500 million people – about a third of the world's population at the time – in four successive waves.

THE COVID IN SPAIN WAS NOT FOUND IN THE DRAIN

EVIDENCE FOR THE EARLY OCCURRENCE OF SARS-COV-2 FROM OTHER STUDIES

"It remains to be determined where SARS-CoV-2 originated. Although the virus was first identified as the cause of a cluster of cases of severe pneumonia in Wuhan, to date it is uncertain from where the first cases originated. A few studies suggest that cases may have occurred before December 2019, the time when circulation of SARS-CoV-2 was thought to have started in Hubei Province. **In a retrospective survey, sewage samples collected on 12 March 2019 in Barcelona, Spain, were positive for SARS-CoV-2 RNA, but other samples collected between January 2018 and December 2019 were all negative.** The PCR signals has not been confirmed by sequencing and could be false-positive signals. Collectively, these studies from different countries suggest that SARS-CoV-2 circulation preceded the initial detection of cases by several weeks. Some of the suspected positive samples were detected even earlier than the first case in Wuhan, suggesting that circulation of the virus in other regions had been missed. So far, however, the study findings were not confirmed, methods used were not standardized, and serological assays may suffer from non-specific signals. Nonetheless, it is important to investigate these potential early events."

https://www.ub.edu/web/ub/en/menu_eines/noticies/2020/06/042.html

THE FROZEN FOOD THEORY LACKS ONE THING - THERE WOULD HAVE BEEN COVID CASES IN BARCELONA, SPAIN, BEFORE THE ONES IN HUANAN BROKE OUT

"Three recent COVID-19 outbreaks in China have been linked to exposure to imported refrigerated or frozen seafood products.(27-30) An outbreak in Beijing linked to the Xinfadi market was first identified on 11 June 2020 after 56 days without a single known community case of COVID-19 in Beijing. Full genome sequencing and phylogenetic analysis of publicly available genomes suggests that the virus was from the L lineage European branch 1 with specific mutations characteristic to the market outbreak. However, it is not possible to fully infer the source of contamination from this work yet. In October 2020, an outbreak occurred in Qingdao. The index cases for the cluster were two dock workers from the city's port with no history of travel or recognized contact with anyone with confirmed COVID-19; the only epidemiological link which could be established between the cases was exposure to SARS-CoV-2 on the surface of cold-chain packaging. In addition, SARS-CoV-2 viruses were isolated from swabs of the outside surfaces of imported cold-chain packages in Qingdao. Based on these observations, China has launched a programme for systematic screening of packaged frozen imported food. Although re-introduction of a pandemic virus to epidemic-free areas can occur via various transmission routes including imported goods during a pandemic, the similarities between the outbreaks in the Beijing Xinfadi market and Qingdao, leading to the consideration of potential introduction of the virus through frozen products into the Huanan market in late 2019. For research focusing on the origin of SARS-CoV-2, this will need to be aligned with sources of those products. The proportion of cases in stalls with cold-chain goods (5.6%) is significantly higher than those without cold-chain goods (1.7%), and the relative risk of cases in stalls with cold-chain goods is 3.3 times higher than those without cold-chain goods (relative risk = 3.3, 95% CI:1.2-8.6), and the morbidity rate of vendors of cold-chain products is higher than others (3.3% compared with 1.4%), but there is no statistically significant difference. Epidemiological analysis showed that the first three cases in Huanan market all had a history of exposure to cold chain."

TYPE OF GOODS DEALT BY ENVIRONMENTAL POSITIVE STALLS / RETROSPECTIVE STUDY ON THE COLD CHAIN IN 2019

"Analyses show that 60% (44/73) of the positive samples are related to 21 stalls, 19 of which were located in the western part of the Huanan market, and the remaining two stalls were located in the eastern part. 16 stalls were dealing with cold-chain product." An inventory was made of imported cold-chain products in large and medium-sized cold warehouses in Wuhan from September to December 2019. It has been confirmed that cold-chain products were still in stock during the above period. From 4-6 February 2021, samples were collected and SARS-CoV-2 NAT were performed on a total of 1055 samples of imported cold-chain food products (no domestic-origin cold chain products could be located at that time) including 330 pieces with outer packages, 244 pieces with inner packages and 481 food samples. The results of SARS-CoV-2 NAT were all negative."

THE PERSISTENCE OF LIVE SARS-COV-2 IN ENVIRONMENTS RELATED TO THE COLD-CHAIN / EXAMPLES OF INTRODUCTION OF COVID-19 INTO CHINA THROUGH IMPORTED COLD CHAIN PRODUCTS

"It was noted that in one study, the infectivity of SARS-CoV-2 on cold-chain products did not decline after 21 days at 4 °C (refrigerated food) or at -20 °C (frozen food). Even at 21-23 °C, SARS-CoV-2 on cardboard surface remained infective up to 24 hours. After China successfully controlled the COVID-19 epidemic in Wuhan in April 2020, a series of clustered epidemics occurred in various places. According to the experience of prevention and control of these epidemics, especially the successful traceability results of Xinfadi in June, Dalian in July and Qingdao in October 2020, it is confirmed that SARS-CoV-2 can survive and maintain infection activity in cold chain products and packaging for a long time, which provides a scientific basis for the possibility of introduction of SARS-CoV-2 through cold chain products."

CONCLUSIONS

"1. CoVs that are phylogenetically related to SARS-CoV-2 were identified in different animals from different countries, including bats (*Rhinolophus* spp) and customs-seized trafficked Malayan pangolins. Sampling and testing of >1,100 bats in Hubei Province, however, has been conducted but none were positive for viruses close to SARS-CoV-2. Sampling of wildlife across China has been conducted but no samples were positive for SARS-CoV-2.

2. The Huanan market had evidence of extensive sale of **frozen products**, fresh sea and aquatic animals and products, livestock meat, and limited farmed wildlife products. All the product samples retrieved during the outbreak investigation tested negative for the SARS-CoV-2 nucleic acid.

3. **SARS-CoV-2 can persist in conditions found in frozen food, packaging and cold-chain products.** Index cases in recent outbreaks in China have been linked to the imported cold chain. These indicate a possibility of transmission of SARS-CoV-2 through frozen products. The supply chains to the markets in Wuhan included cold-chain products (including the seafood, aquatic products, vegetables, animal products and farmed wildlife products) from several provinces in China and 20 other countries. Suppliers included countries and regions where SARS-CoV-2 (NAT and serum) tested positive before the outbreak of SARS-CoV-2, countries where cold chain imported products were sourced, provinces where domestic wildlife farms were sourced, and where the relatives of SARS-CoV-2 are found in bats and pangolins. There is evidence that some domesticated wildlife species sold in the Huanan market are susceptible to SARS-CoV-2 or SARS-CoV, but none of the animal products sampled in the market tested positive. Apart from frozen farmed wildlife products, cold-chain products in Huanan market were not tested specifically in early 2020. These findings do, however, raise the possibility for different potential pathways of introduction, stressing the need for careful trace-back of these supply chains and sample testing.

4. Preliminary sampling and testing at other markets in Wuhan and upstream suppliers to the Huanan market taken during 2020 did not reveal evidence of SARS-CoV-2 circulating in animals. Evidence was not found of presence of SARS-CoV-2 among animal products in the Huanan market and upstream suppliers.

5. Environmental sampling in the Huanan market demonstrated widespread contamination of surfaces with SARS-CoV-2, compatible with the virus shedding from infected people in the market at the end of December 2019. However, through extensive testing of animal products in the market, no evidence of animal infections was found. One environmental sample collected on Jan 22, 2020 on a second market tested positive, implying an environmental contamination from the patients in the communities.

6. Of 923 environmental samples in Huanan market 73 were positive; Forty-four of those positive were from the stalls of 21 vendors dealing in the following products: aquatic animals and products (n = 13), cold-chain products (n = 16), poultry meat (n = 6), seafood products (n = 6), livestock meat (n = 5), vegetable products (n = 2) and farmed wildlife meat (n = 1). Sampling and testing of 38 515 livestock and poultry samples and 41 696 wild animal samples from 31 provinces in China during 2018 to 2020 resulted in no positive SARS-CoV-2 antibody or nucleic acid tests. No evidence was found of circulation of SARS-CoV-2 among domestic livestock, poultry and wild animals before and after the SARS-CoV-2 outbreak in China."

THE BARCELONA WASTE WATER SAMPLES WERE TESTED AFTER THE PANDEMIC BEGAN AND ONLY A MARCH 2019 SAMPLE PROVED POSITIVE FOR SARS CoV-19 INDICATED THE SAMPLE WAS CONTAMINATED IN THE LAB

By searching for, and then counting, certain coronavirus genes in sewage, researchers hoped to determine whether the virus was present in a particular region and how widespread it was: Although Covid-19 is primarily a respiratory disease, research conducted early in the pandemic revealed that people infected with the coronavirus often shed it in their stool. This finding, combined with the scale and urgency of the crisis, spurred immediate interest in tracking the virus by sampling wastewater.

In a study not yet published in a journal, scientists have reported that the new coronavirus was present in wastewater in Barcelona, Spain in March 2019, a finding that, if confirmed, would show that the pathogen had emerged much earlier than previously thought. But independent experts who reviewed the findings said they doubted the claim. The study was flawed, they said, and other lines of evidence strongly suggest the virus emerged in China late last year. Up until now, the earliest evidence of the virus anywhere in the world has been from December 2019 in China and it was only known to have hit mainland Spain in February 2020. "Barcelona is a city that is frequented by Chinese people, in tourism and business, so probably this happened also elsewhere, and probably at the same time," said the lead author, Albert Bosch, a professor in the Department of Microbiology of the University of Barcelona who has been studying viruses in wastewater for more than 40 years. Several experts not involved in the research pointed out problems with the new study, which has not yet been subjected to the critical review by outside experts that occurs before publication in a scientific journal. They suggested that the tests might very well have produced false positives because of contamination or improper storage of the samples. "I don't trust the results," said Irene Xagoraki, an environmental engineer at Michigan State University.

<https://www.nytimes.com/2020/06/26/health/coronavirus-spain.html>

In 2017 Spain was only authorized to export frozen meat and offal and deboned ham to China. A new protocol changes everything, allowing China to import a much larger range of products from Spain, including chilled fresh meat and cured meats such as chorizo, salchichón, ham and shoulder.





THE HUNAN MARKET ORIGIN THEORY DEBUNKED BY W.H.O.

"Many of the early cases were associated with the Huanan market, but a similar number of cases were associated with other markets and some were not associated with any markets. Transmission within the wider community in December 2019 could account for cases not associated with the Huanan market which, together with the presence of early cases not associated with that market, could suggest that the Huanan market was not the original source of the outbreak. Other milder cases that were not identified, however, could provide the link between the Huanan market and early cases without an apparent link to the market."

"The animal and environment working group reviewed existing knowledge on coronaviruses that are phylogenetically related to SARS-CoV-2 identified in different animals, including horseshoe bats (*Rhinolophus* spp) and pangolins. However, the presence of SARS-CoV-2 has not been detected through sampling and testing of bats or of wildlife across China. More than 80 000 wildlife, livestock and poultry samples were collected from 31 provinces in China and no positive result was identified for SARS-CoV-2 antibody or nucleic acid before and after the SARS-CoV-2 outbreak in China. Through extensive testing of animal products in the Huanan market, no evidence of animal infections was found."

W.H.O.- INTRODUCTION THROUGH A LABORATORY INCIDENT

EXPLANATION OF HYPOTHESIS

W.H.O. - SARS-COV-2 IS INTRODUCED THROUGH A LABORATORY INCIDENT, REFLECTING AN ACCIDENTAL INFECTION OF STAFF FROM LABORATORY ACTIVITIES INVOLVING THE RELEVANT VIRUSES. WE DID NOT CONSIDER THE HYPOTHESIS OF DELIBERATE RELEASE OR DELIBERATE BIOENGINEERING OF SARS-COV-2 FOR RELEASE, THE LATTER HAS BEEN RULED OUT BY OTHER SCIENTISTS FOLLOWING ANALYSES OF THE GENOME. [What other scientists?]

ARGUMENTS IN FAVOR OF INTRODUCTION THROUGH A LABORATORY INCIDENT

"Although rare, laboratory accidents do happen, and different laboratories around the world are working with bat CoVs. When working in particular with virus cultures, but also with animal inoculations or clinical samples, humans could become infected in laboratories with limited biosafety, poor laboratory management practice, or following negligence. The closest known CoV RaTG13 strain (96.2%) to SARS-CoV-2 detected in bat anal swabs have been sequenced at the Wuhan Institute of Virology. The Wuhan CDC laboratory moved on December 2, 2019 to a new location near the Huanan market. Such moves can be disruptive for the operations of any laboratory."

ARGUMENTS AGAINST INTRODUCTION THROUGH A LABORATORY INCIDENT

"The closest relatives of SARS-CoV-2 from bats and pangolin are evolutionarily distant from SARS-CoV-2. There has been speculation regarding the presence of human **ACE2** receptor binding and a furin-cleavage site in SARS-CoV-2, but both have been found in animal viruses as well, and elements of the furin-cleavage site are present in RmYN02 and the new Thailand bat SARSr-CoV.¹ There is no record of viruses closely related to SARS-CoV-2 in any laboratory before December 2019, or genomes that in combination could provide a SARS-CoV-2 genome. Regarding accidental culture, prior to December 2019, there is no evidence of circulation of SARS-CoV-2 among people globally and the surveillance programme in place was limited regarding the number of samples processed and therefore the risk of accidental culturing SARS-CoV-2 in the laboratory is extremely low. The three laboratories in Wuhan working with either CoVs diagnostics and/or CoVs isolation and vaccine development all had high quality biosafety level (BSL3 or 4) facilities that were well-managed, with a staff health monitoring programme with no reporting of COVID-19 compatible respiratory illness during the weeks/months prior to December 2019, and no serological evidence of infection in workers through SARS-CoV-2-specific serology-screening. The Wuhan CDC lab which moved on 2nd December 2019 reported no disruptions or incidents caused by the move. They also reported no storage nor laboratory activities on CoVs or other bat viruses preceding the outbreak."

1. [The ACE2 receptor binding and a furin-cleavage site in animals is non-infectious.](#)

ASSESSMENT OF LIKELIHOOD

In view of the above, a laboratory origin of the pandemic was considered to be extremely unlikely. What would be needed to increase knowledge? Regular administrative and internal review of high-level biosafety laboratories worldwide. Follow-up of new evidence supplied around possible laboratory leaks.

REFERENCES IN W.H.O. REPORT INDICATE ANDERSON INTERFACES WITH ECOHEALTH

- (1) [Likert R. \(1932\). A technique for the measurement of attitudes. Archives of Psychology. 140:44–53.](#)
- (2) Kenneth J. Olival, Parvaz Hosseini, Carlos Zambrana-Torrel et al. Host and viral traits predict zoonotic spillover from mammals. **Nature** **546**, 646–650 (2017)
- (3) [Kristain G Andersen](#) Rambaut A, Lipkin WI, **Edward C. Holmes**, and [Garry Robert F \(2020\)](#). The proximal origin of SARS-CoV-2. *Nature Medicine* 26:450–452

1. Author information Affiliations EcoHealth Alliance, 460 West 34th Street, New York, 10001, New York, USA Kevin J. Olival, Parvaz R. Hosseini, Carlos Zambrana-Torrel, Noam Ross, Tiffany L. Bogich & Peter Daszak

"Coronavirus Update: Study Finds 781 Coronaviruses In Bats In China." *Business Times - US ed.* Date FEBRUARY 6, 2020 Persons **Peter Daszak**, **Edward C. Holmes** <https://covid19.elsevierpure.com/en/clippings/coronavirus-update-study-finds-781-coronaviruses-in-bats-in-china>

Nature Magazine: "That the WIV, a laboratory highly regarded for its work on bat coronaviruses, is located in the city where the outbreak first emerged is probably just a coincidence." <https://www.nature.com/articles/d41586-020-01541-z>

China owns *Nature Magazine*: Debunking “The proximal origin of SARS-CoV-2” claiming COVID-19 definitely wasn’t from a lab
<https://www.insidehighered.com/news/2018/10/03/book-publishers-part-ways-springer-nature-over-concerns-about-censorship-china>

HIGHLIGHTS FROM SHORT W.H.O. REPORT

ENTIRE SHORT REPORT

1. Alignment of the full-length genome sequence of the COVID-19 virus and other available genomes of Betacoronavirus showed the closest relationship was with the bat SARS-like coronavirus strain BatCov RaTG13, identity 96%. [THE SIGNIFICANCE OF THAT 4% DIFFERENCE](#)

2. Transgenic human **ACE2** mice and Rhesus monkey intranasally challenged by this virus isolate induced multifocal pneumonia with interstitial hyperplasia. The COVID-19 virus was subsequently detected and isolated in the lung and intestinal tissues of the challenged animals. [ACE2 AFFINITY INDICATES DESIGNER VIRUS](#)

3. COVID-19 is a zoonotic virus. From phylogenetics analyses undertaken with available full genome sequences, bats appear to be the reservoir of COVID-19 virus, **but the intermediate host (s) has not yet been identified**. However, three important areas of work are already underway in China to inform our understanding of the zoonotic origin of this outbreak. These include early investigations of cases with symptom onset in Wuhan throughout December 2019, environmental sampling from the Huanan Wholesale Seafood Market and other area markets, and the collection of detailed records on the source and type of wildlife species sold at the Huanan market and the destination of those animals after the market was closed...**Early cases identified in Wuhan are believed to have acquired infection from a zoonotic source as many reported visiting or working in the Huanan Wholesale Seafood Market. As of 25 February, an animal source has not yet been identified.** [MORE ON THE WUHAN MARKET MYTH](#)

4. Airborne spread has not been reported for COVID-19 and it is not believed to be a major driver of transmission based on available evidence; however, it can be envisaged if certain aerosol-generating procedures are conducted in health care facilities. Nationally, wildlife markets were closed and wildlife captive-breeding facilities were cordoned off.¹

1. More of the Daszak CHI-COM animal to market to human CCP LINE.

Similarly, there is a long list of proposed studies on the origins of COVID-19, the natural history of the disease, and the virus's transmission dynamics. However, the urgency of responding to cases and saving lives makes it difficult for policy makers to consider and act on such comprehensive lists.¹

1. In other words we must postpone any further investigation of the origin of COV-2 for the distant future..

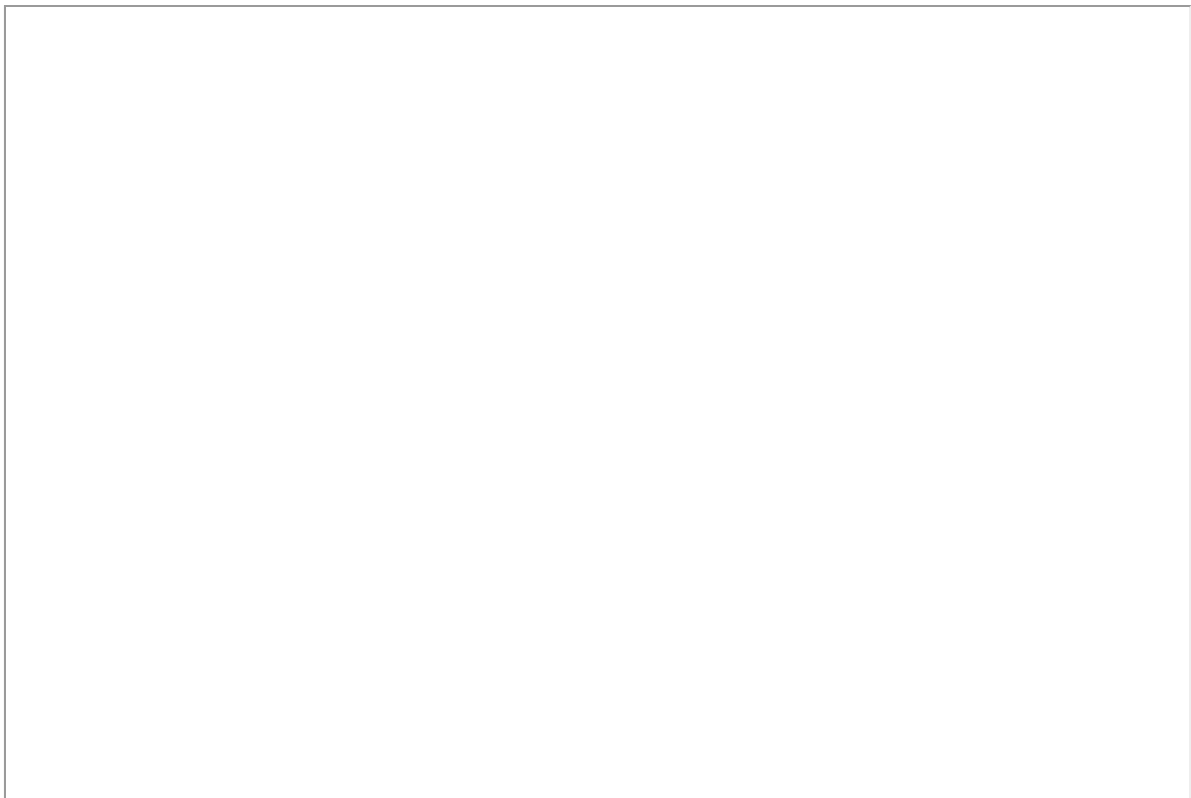
W.H.O. REPORT IS A BIG NOTHING BURGER

D. Knowledge Gaps Knowledge gaps and key questions to be answered to guide control strategies include:

Source of infection

- Animal origin and natural reservoir of the virus
- Human-animal interface of the original event
- Early cases whose exposure could not be identified

USG REJECTS WHO INVESTIGATION



WALL STREET JOURNAL: SCIENTISTS REJECT COVID-COVER-UP ORCHESTRATED BY DASZAK



DASZAK IN THE COUNTRY HE IS LOYAL TO

MARCH 4, 2021 BEIJING—A World Health Organization team investigating the origins of Covid-19 is planning to scrap an interim report on its recent mission to China amid mounting tensions between Beijing and Washington over the investigation and an appeal from one international group of scientists for a new probe. The group of two dozen scientists is calling **in an open letter** on Thursday for a new international inquiry. They say the W.H.O. team that last month completed **a mission to Wuhan**—the Chinese city where the first known cases were found—had insufficient access to adequately investigate possible sources of the new coronavirus, including whether it slipped from a laboratory. Their appeal comes as the U.S.—which recently reversed a decision to leave the W.H.O.—**lobbies for greater transparency** in the investigation, saying it is waiting to scrutinize the report on the Wuhan mission, and urging China to release all relevant data, including on the first confirmed infections in December 2019, and **potential earlier ones**. Beijing, meanwhile, is pressing for similar W.H.O.-led missions to other countries, including the U.S., to investigate whether the virus could have originated outside China and spread to Wuhan **via frozen food packaging**. W.H.O. chief Tedros Adhanom Ghebreyesus **said on Feb. 12** that the team would release an interim report briefly summarizing the Wuhan mission, possibly the following week, with a full report coming weeks later. But that summary report has yet to be published and the W.H.O. team is now scrapping that plan, said Peter Ben Embarek, the food-safety scientist who led the team. The W.H.O. team plans to publish a summary along with the full, final report, he said. That final report “will be published in coming weeks and will include key findings,” a W.H.O. spokesman said. ALSO SEE <https://int.nyt.com/data/documenttools/covid-origins-letter/5c9743168205f926/full.pdf>

MARCH 21, 2021 [60 Minutes: Daszak sticks to discredited Wuhan Market theory](#)

CHAPTER 25

INVESTIGATE THE ORIGINS OF COVID-19

MAY 14, 2021 More than one year after the breakout these “courageous” microbiologists are finally calling for lab leak investigation.

Jesse D. Bloom 1,2, Yujia Alina Chan 3, Ralph S. Baric 4, Pamela J. Bjorkman 5, Sarah Cobey 6, Benjamin E. Deverman 3, David N. Fisman 7, Ravindra Gupta 8, Akiko Iwasaki 9,2, Marc Lipsitch 10, Ruslan Medzhitov 9,2, Richard A. Nehe r11, Rasmus Nielsen 12, Nick Patterson 13, Tim Stearns 14, Erik van Nimwegen 11, Michael Worobey 15, David A. Relman 16,17,*

1. Basic Sciences and Computational Biology, Fred Hutchinson Cancer Research Center, Seattle, WA 98109, USA.
 2. Howard Hughes Medical Institute, Chevy Chase, MD 20815, USA.
 3. Stanley Center for Psychiatric Research, Broad Institute of Massachusetts Institute of Technology and Harvard University, Cambridge, MA 02142, USA.
 4. Department of Epidemiology and Department of Microbiology & Immunology, University of North Carolina at Chapel Hill, Chapel Hill, NC 27599, USA.
 5. Division of Biology and Biological Engineering, California Institute of Technology, Pasadena, CA 91125, USA.
 6. Department of Ecology and Evolution, University of Chicago, Chicago, IL 60637, USA.
 7. Dalla Lana School of Public Health, University of Toronto, Toronto, ON M5S 1A8, Canada.
 8. Cambridge Institute of Therapeutic Immunology & Infectious Disease, Cambridge, UK.
 9. Department of Immunobiology, Yale University School of Medicine, New Haven, CT 06519, USA.
 10. Department of Immunology and Infectious Diseases and Center for Communicable Disease Dynamics, Department of Epidemiology, Harvard T. H. Chan School of Public Health, Boston, MA 02115, USA.
 11. Biozentrum, University of Basel and Swiss Institute of Bioinformatics, Basel, Switzerland.
 12. Department of Integrative Biology and Department of Statistics, University of California, Berkeley, CA 94720, USA.
 13. Department of Human Evolutionary Biology, Harvard University, Cambridge, MA 02138, USA.
 14. Department of Biology and Department of Genetics, Stanford University, Stanford, CA 94305, USA.
 15. Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, AZ 85721, USA.
 16. Department of Medicine and Department of Microbiology & Immunology, Stanford University School of Medicine, Stanford, CA 94305, USA.
 17. Center for International Security and Cooperation, Stanford University, Stanford, CA 94305, USA.
- * Corresponding author. Email: relman@stanford.edu



GO BACK

FRANCIS COLLINS THE TALKING MULE

FRANK COLLINS CLAIMS NEITHER NIH NOR NIAID HAVE EVER APPROVED ANY GRANT THAT WOULD HAVE SUPPORTED GAIN-OF-THREAT RESEARCH ON CORONAVIRUSES THAT WOULD HAVE INCREASED THEIR TRANSMISSIBILITY OR LETHALITY FOR HUMANS

MAY 19, 2021 Statement on misinformation about NIH support of specific Gain-of-Function” research. Based on outbreaks of coronaviruses caused by animal to human transmissions such as in Asia in 2003 that caused Severe Acute Respiratory Syndrome(link is external) (SARS), and in Saudi Arabia in 2012 that caused Middle East Respiratory Syndrome(link is external) (MERS), NIH and the National Institute of Allergy and Infectious Diseases (NIAID) have for many years supported grants to learn more about viruses lurking in bats and other mammals that have the potential to spill over to humans and cause widespread disease. **However, neither NIH nor NIAID have ever approved any grant that would have supported “gain-of-function” research on coronaviruses that would have increased their transmissibility or lethality for humans.** NIH strongly supports the need for further investigation by the World Health Organization (WHO) into the origins of the SARS-CoV-2 coronavirus. Working with a cross-regional coalition of 13 countries(link is external), we urge the W.H.O. to begin the second phase of their study without delay. Francis S. Collins, M.D., Ph.D. Director, National Institutes of Health

<https://www.nih.gov/about-nih/who-we-are/nih-director/statements/statement-misinformation-about-nih-support-specific-gain-function-research>

MAY 21, 2021 The Wuhan Institute of Virology disclosed the genomic sequences of eight new viruses that were the second, third, fourth, fifth, sixth, seventh, eighth and ninth genetically closest viruses to SARS-CoV-2. Their full sequences were only disclosed on May 21, even though the viruses were obtained from a mine in Mojiang in 2015 – the same mine where RaTG13, a virus that shares a 96 per cent sequence identity with Covid-19, was found.

Severe respiratory disease coronavirus-2 (SARS-CoV-2) causes the most devastating disease, COVID-19, of the recent century. One of the unsolved scientific questions around SARS-CoV-2 is the animal origin of this virus. Bats and pangolins are recognized as the most probable reservoir hosts that harbor the highly similar SARS-CoV-2 related viruses (SARSr-CoV-2). Here, we report the identification of a novel lineage of SARSr-CoVs, including RaTG15 and seven other viruses, from bats at the same location where we found RaTG13 in 2015. Although RaTG15 and the related viruses share 97.2% amino acid sequence identities to SARS-CoV-2 in the conserved ORF1b region, but only show less than 77.6% to all known SARSr-CoVs in genome level, thus forms a distinct lineage in the Sarbecovirus phylogenetic tree. We then found that RaTG15 receptor binding domain (RBD) can bind to and use Rhinolophus affinis bat ACE2 (RaACE2) but not human ACE2 as entry receptor, although which contains a short deletion and has different key residues responsible for ACE2 binding. **In addition, we show that none of the known viruses in bat SARSr-CoV-2 lineage or the novel lineage discovered so far use human ACE2 efficiently compared to SARSr-CoV-2 from pangolin or some of the SARSr-CoV-1 lineage viruses.** Collectively, we suggest more systematic and longitudinal work in bats to prevent future spillover events caused by SARSr-CoVs or to better understand the origin of SARS-CoV-2.

<https://www.biorxiv.org/content/10.1101/2021.05.21.445091v1>

STATEMENT BY PRESIDENT JOE BIDEN ON THE INVESTIGATION INTO THE ORIGINS OF COVID-19

MAY 26, 2021 “Back in early 2020, when COVID-19 emerged, I called for the CDC to get access to China to learn about the virus so we could fight it more effectively. The failure to get our inspectors on the ground in those early months will always hamper any investigation into the origin of COVID-19. Nevertheless, shortly after I became President, in March, I had my National Security Advisor task the Intelligence Community to prepare a report on their most up-to-date analysis of the origins of COVID-19, including whether it emerged from human contact with an infected animal or from a laboratory accident. I received that report earlier this month, and asked for additional follow-up. As of today, the U.S. Intelligence Community has “coalesced around two likely scenarios” but has not reached a definitive conclusion on this question. Here is their current position: “while two elements in the IC leans toward the former scenario and one leans more toward the latter – each with low or moderate confidence – the majority of elements do not believe there is sufficient information to assess one to be more likely than the other.” I have now asked the Intelligence Community to redouble their efforts to collect and analyze information that could bring us closer to a definitive conclusion, and to report back to me in 90 days. As part of that report, I have asked for areas of further inquiry that may be required, including specific questions for China. I have also asked that this effort include work by our National Labs and other agencies of our government to augment the Intelligence Community’s efforts. And I have asked the Intelligence Community to keep Congress fully apprised of its work. The United States will also keep working with like-minded partners around the world to press China to participate in a full, transparent, evidence-based international investigation and to provide access to all relevant data and evidence.”

<https://www.whitehouse.gov/briefing-room/statements-releases/2021/05/26/statement-by-president-joe-biden-on-the-investigation-into-the-origins-of-covid-19>

The leaders of the world’s wealthiest large democracies, at the Group of 7 summit, urged China to be part of a new investigation into the origins of the coronavirus. Mr. Biden told reporters that he and other leaders had discussed access to labs in China. This investigation is going to be a cover-up. The implications of a leak at the WIV are too far reaching and trace back to Baric and

Daszak and others including Fauci. And no one wants to mess with China. Philip D. Zelikow investigation is also going to be a cover-up since he is a former CIA agent who worked under diplomatic cover.

MAY 2021 David Relman, a prominent microbiologist at Stanford: "There are lots of cases where viruses go from bats to humans." But there were a number of reasons why the possibility of a lab leak remained viable. Chinese scientists have reportedly tested fifty thousand samples from three hundred species of wildlife, searching for the missing link, and hadn't yet found one carrying sars-CoV-2. "The fact is, no one has found sars-CoV-2 anywhere other than in humans,"
[newyorker.com/news/annals-of-inquiry/the-sudden-rise-of-the-coronavirus-lab-leak-theory](https://www.newyorker.com/news/annals-of-inquiry/the-sudden-rise-of-the-coronavirus-lab-leak-theory)

CCP MOUTHPIECE GLOBAL TIMES: US INTELLIGENCE INVESTIGATION OF CORONAVIRUS ORIGINS EXPOSES ITS FOUR 'ACHILLES HEELS'

MAY 30, 2021 The CCP: "As for the so-called undisclosed US intelligence report that some Wuhan researchers were infected by COVID-19 before an epidemic was confirmed, Dutch virologist **Marian Koopmans** attributed that to regular, seasonal sickness as early as in March. US intelligence agencies do not have superior research capability than the W.H.O., nor did they have more information. What they will get in the end is nothing but political. They will have to make a political decision either to produce a slanderous report that is in line with the US' anti-China campaign, or to step back in front of mainstream opposition from scientists and do their best to save the reputation of the US government that is already stuck in a dilemma."
<https://www.globaltimes.cn/page/202105/1224896.shtml>



PETER DASZAK / MARIAN KOOPMANS

Marian Koopmans studied veterinary medicine at Utrecht University. She graduated from her Master's degree 1976, and remained there for her doctoral research. She earned two graduate degrees in veterinary medicine, and was officially registered as a veterinary microbiologist in 1977. She serves on the scientific advisory group of the **World Health Organization**. She co-authored papers with Fouchier, R.A.M. (Ron) Genetic adaptation of influenza A viruses in domestic animals and their potential role in interspecies transmission: a literature review O Munoz, M De Nardi, K van der Meulen, K Van Reeth, **Marian Koopmans**, ...**Ecohealth** 13 , 171-198 Epidemiological risk factors for animal influenza A viruses overcoming species barriers KA Harris, GS Freidl, OS Munoz, S von Dobschuetz, M De Nardi, ...**Ecohealth** 14 (2), 342-360 GENETIC ADAPTATION OF INFLUENZA A VIRUSES IN DOMESTIC ANIMALS AND THEIR POTENTIAL ROLE IN INTERSPECIES TRANSMISSION: A LITERATURE REVIEW (VOL 13, PG 171, 2016) O Munoz, M De Nardi, K Van Der Meulen, K Van Reeth, M Koopmans, ...**Ecohealth** 13
<https://scholar.google.com/citations?user=cwUzg-kAAAAJ>

1998 / 2010 - Population Dynamics and Genetic Diversity of C4 Strains of Human Enterovirus 71 in Mainland China. In samenwerking met: Dawei Guan, Sabine van der Sanden, Hanri Zeng, Wei Li, Huanying Zheng, Cong Ma, Juan Su, Zheng Liu, Xue Guo, Xin Zhang, Leng Liu, Marion Koopmans, Changwen Ke. Plos One September 2012, Volume 7, Issue 9, e44386.

2008 / 2009 - Adamantane- and oseltamivir-resistant seasonal A (H1N1) 2009 influenza viruses in Guangdong, China. In samenwerking met: Zhou J, Zou L, Zhang X, Liao J, Ni H, Hou N, Wang Y, Li H, Wu J, Jonges M, Meijer A, Koopmans M, Ke C. J Clin Microbiol. 2011 Jul;49(7): 2651-5.

2010 december - Annual meeting on laboratory network of emergency responses and surveillance of infectious diseases in Pan Pearl River Delta region 2010, 'Exposure assessment using micro-array based serology', Guangdong China

JUNE 7, 2021 A survey from The Economist/YouGov found 58 percent of Americans said COVID-19 came from a Wuhan lab, up from 49 percent who said the same when the pollsters first asked the question in May of 2020. Meanwhile, 18 percent said it was "definitely or probably false" that the virus came from a Chinese lab, while 24 percent said they didn't know.

JUNE 7, 2021 *Wall Street Journal* runs article conclusively proving SARS-CoV-19 was result of GoF / GoT experiments in WIV.

JULY 5, 2021 [Lancet anti-lab leak theory letter signatories missing Baric and Anderson: However they include Rita Colwell E-HA \(Daszak entity\), Hume Field E-HA, James Hughes E-HA, Jonna Keener Mazet PREDICT, and John S Mackenzie WHO](#)

August 18, 2021 On the net: [The Origins of SARS-CoV-2: A Critical Review...](#) "Origins" article references are bogus. No mention of [furin](#)

W.H.O. WILL ANNOUNCE NEW TEAM TO STUDY CORONAVIRUS ORIGINS

"This new group can do all the fancy footwork it wants, but China's not going to cooperate," David Fidler, a senior fellow for global health at the Council on Foreign Relations.

The new committee, is known as the [Scientific Advisory Group for the Origins of Novel Pathogens](#). After the Sago list was released, proponents of a lab investigation raised concerns – including in open letters to the WHO last week – calling for some nominees to be removed and suggesting the proposed group did not include those with the skills or interest to guide recommendations on how best to evaluate the "lab leak" hypothesis. Beijing has vehemently rejected this theory, which it views as politically motivated and fanned by the US, and has made clear it will not allow further missions to China that seek to audit laboratories. [CCP](#)



CHAPTER 26

TRUMP-FUELED SUSPICION OF WUHAN LAB ENSNARES NEW YORK NONPROFIT RESEARCHING BAT CORONAVIRUSES. WAPO May 12, 2020 By Paul Sonne and Shane Harris

May 12, 2020 Anthony S. Fauci, who runs the part of the National Institutes of Health that awarded EcoHealth's grant and later terminated it, could face questions about the matter during testimony in front of a Senate committee. EcoHealth's work in China first gained national attention during the pandemic when Trump, at a news conference in mid-April, pledged to pull its grant from NIH. Days later, the president's personal attorney, Rudolph W. Giuliani, assailed the grant in a tweet. Neither Trump nor Giuliani mentioned the nonprofit organization by name, instead focusing on its partners in Wuhan. Late last month, NIH followed through on Trump's promise and abruptly pulled more than \$3 million in funding over five years that was awarded in 2019. NIH gave the nonprofit organization little reason for doing so, writing in a letter that the project didn't align with "program goals and agency priorities." But questions about exactly how and where the natural spillover took place, coupled with China's refusal so far to allow an independent investigation into the origins of the pandemic, have bred suspicion about whether the institute could be to blame. So has the coincidence that both the bat coronavirus research and the outbreak took place in the city of Wuhan.... "This idea that it doesn't fit the goals and objectives — there must be more to it," **EcoHealth Alliance President Peter Daszak said in a May 1 interview. "You can't apply for money from the NIH unless it's within the goals and objectives of the organization. They review that when you submit a proposal."** NIH confirmed in a statement that EcoHealth's grant was terminated and acknowledged that the Wuhan Institute of Virology was a "sub-awardee."¹

In other words Daszak "laundered" the grant for Fauci.

"The Office of the Director (OD) of NIAID determines Institute programs, plans, and policies and provides management, program analysis, and scientific program reporting services to the Institute, as well as scientific leadership, policy guidance, and overall operational and administrative coordination. The OD serves as the chief liaison with the National Institutes of Health (NIH) director, other components of the U.S. Department of Health and Human Services (HHS), other federal agencies, Congress, professional societies, voluntary health organizations, and other public health groups. It also coordinates the activities of NIAID extramural and intramural divisions."

Mr. SCIENCE. ANTHONY FAUCI EMAILS

FROM Greg Folkers (NIH/NIA ID) TO Anthony Fauci: *Nature* ran a story in 2017 about it building a new biosafety level 4 lab and included molecular biologist Richard Ebright of Rutgers University, Piscataway, expressing concerns about accidental infections, which he noted repeatedly happened NIH-002400 with lab workers handling SARS in Beijing. Ebright, who has a long history of raising red flags about studies with dangerous pathogens, also in 2015 criticized an experiment in which modifications were made to a SARS-like virus circulating in Chinese bats to see whether it had the potential to cause disease in humans. Earlier this week, Ebright questioned the accuracy of Bedford's calculation that there are at least 25 years of evolutionary distance between RaTG13- the virus held in the Wuhan virology institute - and 2019-nCoV, arguing that the mutation rate may have been different as it passed through different hosts before humans. Ebright tells *Science Insider* that the 2019-nCoV data are "consistent with entry into the human population as a natural accident." Shi did not reply to emails from *Science*, but her longtime collaborator, disease ecologist Peter Daszak of the EcoHealth Alliance, dismissed Ebright's conjecture. **"Every time there's an emerging disease, a new virus, the same story comes out: This is a spillover or the release of an agent or a bioengineered virus. It's just a shame. It seems humans can't resist controversy and these myths, yet it's staring us right in the face. There's this incredible diversity of viruses in wildlife and we've just scratched the surface. Within that diversity, there will be some that can infect people and within that group will be some that cause illness."**

Daszak and Shi's group have for 8 years been trapping bats in caves around China to sample their feces and blood for viruses. He says they have sampled more than 10,000 bats and 2000 other species. They have found some 500 novel coronaviruses, about 50 of which fall relatively close to the SARS virus on the family tree, including RaTG13-it was fished out of a bat fecal sample they collected in 2013 from a cave in Moglang in Yunnan province. "We cannot assume that just because this virus from Yunnan has high sequence identity with the new one that that's the origin," Daszak says, noting that only a tiny fraction of coronaviruses that infect bats have been discovered. "I expect that once we've sampled and sampled across southern China and central China that we're going to find many other viruses and some of them will be closer [to 2019-nCoV]." It's not just a "curious interest" to figure out what sparked the current outbreak, Daszak says. "If we don't find the origin, it could still be a raging infection at a farm somewhere, and once this outbreak dies, there could be a continued spillover that's really hard to stop. But the jury is still out on what the real origins of this are."



Information in this e-mail withheld under (b)(7) records or information compiled for law enforcement purposes, but only to the extent that the production of such law enforcement records or information (A) could be reasonably be expected to interfere with enforcement proceedings.

From: Fauci, Anthony (NIH/NIAD) [E]
Sent: Sun, 19 Apr 2020 03:29:42 +0000
To: Peter Daszak
Subject: RE: Thank you for your public comments re COVID-19's origins

Peter:
Many thanks for your kind note.
Best regards,
Tony

From: Peter Daszak (b) (6)
Sent: Saturday, April 18, 2020 9:43 PM
To: Morens, David (NIH/NIAD) [E] (b) (6); Fauci, Anthony (NIH/NIAD) [E] (b) (6)
Cc: Stemmy, Erik (NIH/NIAD) [E] (b) (6); Erbelding, Emily (NIH/NIAD) [E] (b) (6); Aleksei Chmura (b) (6)
Subject: Thank you for your public comments re COVID-19's origins
Importance: High

Tony (cc'ing David so that you might pass this on to Tony once he has a spare second)

As the PI of the R01 grant publicly targeted by Fox News reporters at the Presidential press briefing last night, I just wanted to say a personal thankyou on behalf of our staff and collaborators, for publicly standing up and stating that the scientific evidence supports a natural origin for COVID-19 from a bat-to-human spillover, not a lab release from the Wuhan Institute of Virology.

(b) (7)(D)

From my perspective, your comments are brave, and coming from your trusted voice, will help dispel the myths being spun around the virus' origins.

Once this pandemic's over I look forward thanking you in person and let you know how important your comments are to us all.

(b) (7)(A)

"I have always said, and will say today to you, [John Berman], that I still believe the most likely origin is from an animal species to a human, but I keep an absolutely open mind that if there may be other origins of that, there may be another reason, it could have been a lab leak. I believe if you look historically, what happens in the animal-human interface, that in fact the more likelihood is that you're dealing with a jump of species. But I keep an open mind all the time. And that's the reason why I have been public that we should continue to look for the origin. You can misconstrue it however you want -- that email was from a person to me saying 'thank you' for whatever it is he thought I said, and I said that I think the most likely origin is a jumping of species. I still do think it is, at the same time as I'm keeping an open mind that it might be a lab leak."

<https://www.cnn.com/2021/06/03/health/anthony-fauci-emails/index.html>

CHAPTER 28

THE ECO-HEALTH ALLIANCE

Call for resignation PDF

The Crypto-Nazi LaRouche residue, whose info must be carefully vetted because it mixes real information with false information, such as Daszak is a British MI-5 Agent, reported: "After Daszak came to the United States and volunteered for the CDC, he joined

and led the [Consortium of Conservation Medicine \(CCM\) beginning in 2004](#). CCM, and its successor, EcoHealth Alliance, is a post-modern concoction combining eco-fascism and public health. CCM works to prevent the development of new infrastructure projects within impoverished nations to ostensibly “stop the spread of disease.” This means they prevent development such as energy, water, and sanitation projects, which are the very foundations for the miracle of modern public health. Instead, CCM looks to cultivate a catalogue of potential new viruses while protecting their natural reservoirs. Here is what their [own website](#) says: “Wild animals like bats and rodents are the natural reservoir for zoonotic pathogens and have carried these pathogens for thousands of years. They are not to blame for these disease emergence events—it is humans who are responsible for altering the environment and increasing contact and conflict with these important species.” By 2010 Daszak’s Consortium of Conservation Medicine joined with an operation called the Royal Society of Wildlife Trust, which was initially established by Gerald Durrell as The [Wildlife Preservation Trust International](#) in 1963, and with the Dodo bird as its symbol, is still run from the Crown’s Channel Island of Jersey. The Royal Society of Wildlife Trust, set up in 1999, is now an organization of forty-six different wildlife trusts operated from the Crown’s Channel Islands of Man and Alderney. [EIR - LaRouche](#) Also see: [ECO-HEALTH ABOUT](#)

RE-BRANDING PRESS RELEASE

Wildlife Trust is a nonprofit organization that began in 1971 with a focus on wildlife conservation, but over the past 20 years, the organization has expanded its focus to include conservation medicine based on research about the relationships between ecosystems and animal and human health around the world. Throughout the past two years, the organization’s board of directors, staff and alliance members have been working on rebranding Wildlife Trust, and today, the new brand was introduced officially via a press release. Wildlife Trust has been renamed as EcoHealth Alliance with a new website and slogan: “Local Conservation, Global Health.” The goal of the rebranding effort is to more accurately present the organization’s dual focus on local wildlife conservation and it’s ongoing leadership in the area of conservation medicine and the relationships between animal ecosystems and human health. The effort won’t stop with a new name, logo and website. EcoHealth Alliance is also hiring new scientists, forming new alliance partnerships, and developing more programs to support the brand’s dual focus. As the EcoHealth Alliance website explains: EcoHealth Alliance works at the intersection of ecosystem, animal and human health through local conservation programs and develops global health solutions to emerging diseases.” Furthermore, EcoHealth Alliance is marketing its new brand focus with messaging that positions the organization as being on, “the forefront of informing the public, businesses, and the scientific community about emerging diseases, including potential pandemics.”

COMMENT: If it was the organization’s goal to shift its brand focus, then one would think that they made a wise strategic move in rebranding to better promote their efforts related to health and medicine. To the average individual, the Wildlife Trust was very much rooted in wildlife conservation with the masses knowing very little about the organization’s other priorities. The new branding puts health and medicine center stage with wildlife conservation taking a back seat. It appears that this was the intent of the rebranding effort, and if that’s true, then the rebranding should work well. What do you think? Does the rebranding work? When you look at the new logo and hear the new brand name, do you still think of wildlife conservation or has the entire brand promise shifted with this rebranding effort? I’m leaning toward the latter. I wonder if that was truly the organization’s intent. [www.corporate-eye.com](#)

[WILD LIFE TRUSTS](#) is the trading name of the Royal Society of Wildlife Trusts, is an organisation made up of 46 local Wildlife Trusts in the United Kingdom, the Isle of Man and Alderney. The Wildlife Trusts, between them, look after more than 2,300 nature reserves, covering around 98,500 hectares (243,000 acres). As of 2020, the Trusts have a combined membership of over 850,000 members. The Royal Society of Wildlife Trusts (RSWT) is an independent charity, with a membership formed of the 46 individual charitable Trusts. It acts as an umbrella group for the individual Wildlife Trusts, as well as operating a separate Grants Unit which administers a number of funds. Charles, Prince of Wales serves as the patron of the Wildlife Trusts. David Bellamy was president of The Wildlife Trusts for ten years between 1995 and 2005, [Foundation Money](#)

Doctor Richard Ebright, the foremost authority on biological warfare in the U.S., has been on to incalculable dangers of conducting Gain-of-Threat experiments. He had provided valuable information on the EcoHealth Alliance:



CHAPTER 29

THE ECO-HEALTH ALLIANCE GRANTS



ECO-HEALTH ALLIANCE scam was just another money making operation that got millions in USG grants. The FBI was unable to identify records responsive to my request [#1495656-000 5/4/21]. Daszak' Eco-Health Alliance's operations need to be examined by congress. His bogus programs that didn't predict COVID-19 in fact it produced it!. Daszak's Ecohealth Alliance diverted \$600,000 in grants from U.S. National Institutes of Health to the WIV between 2014 and 2019 to outsource gain-of-function / gain-of-threat experiments with bat coronaviruses.

<https://www.usaspending.gov/search/? hash=29bacd91b448e1783d9e225844f469c7>

Recipient Name ▼	Start Date ▼	End Date ▼	Award Amount (Total Award Obligations to Date)
ECOHEALTH ALLIANCE INC.	10/2/2017	10/1/2022	\$6,491,025
ECOHEALTH ALLIANCE INC.	7/1/2020	6/30/2025	\$4,995,106
ECOHEALTH ALLIANCE INC.	8/19/2019	8/1/2024	\$4,988,987
ECOHEALTH ALLIANCE INC.	6/1/2020	5/31/2025	\$4,912,818
ECOHEALTH ALLIANCE INC.	6/1/2014	6/30/2025	\$3,748,715
ECOHEALTH ALLIANCE INC.	8/1/2002	6/30/2013	\$3,725,160
ECOHEALTH ALLIANCE INC.	9/25/2020	9/24/2023	\$2,962,906
ECOHEALTH ALLIANCE INC.	9/29/2020	9/28/2023	\$2,956,309
ECOHEALTH ALLIANCE INC.	5/28/2014	5/27/2017	\$2,942,019
ECOHEALTH ALLIANCE INC.	9/18/2008	8/31/2013	\$2,579,553
ECOHEALTH ALLIANCE INC.	9/18/2013	2/28/2019	\$2,499,147
ECOHEALTH ALLIANCE INC.	5/28/2014	5/27/2019	\$1,994,340
ECOHEALTH ALLIANCE INC.	5/1/2017	4/30/2019	\$1,604,523

The Financial Paper Trail Connecting the Gain-of-Function Research paid to Peter Daszak at EcoHealth.

SUMMARY

FEDERAL GRANTS & CONTRACTS

AGENCY	TOTAL
DoD** Department of Defense	\$38,949,941.00 2013-2020
HHS** Health & Human Services	\$13,023,168.00 2007-2020
NSF National Science Foundation	\$2,590,418.00 2006-2020
USAID U.S. Agency for International Development	\$2,499,147.00 2013-2016
DHS Department of Homeland Security	\$2,272,813.00 2016-2019
DoC Department of Commerce	\$1,241,933.00 2006-2010
USDA U.S. Department of Agriculture	\$646,701.00 2007-2009
DoI Department of the Interior	\$267,062.00 2004-2014
GRAND TOTAL	\$61,491,183.00

** Includes NIH and CDC.

*** Also provided "Policy Advisor" David Franz. Former Commander for Fort Detrick - Principal U.S. Government Bioware/Biodefense Facility.

Compensation of Leaders			
(FYE 06/2019)			
Compensation	% of Expenses	Paid to	Title
\$354,065	2.13%	Peter Daszak	President

Program Name	Amount Spent	% of Program Expenses
USAID Predict Emerging Pandemic Threat (EPTP)	\$12,569,067	83.4%
RVF Virus Investigation	\$1,134,848	7.5%
Biological Surveillance	\$679,507	4.5%



Recipient Information



ECOHEALTH ALLIANCE INC

- **Address:** 1200 LINCOLN AVENUE PROSPECT PARK, NY 10001
- **County:** NEW YORK
- **Country:** United States of America
- **Type:** Supplier Organizations (Service, Supplies, Material and Equipment)
- **Class:** Private Profit (Small Business) Organizations

HIDE MAP

ECOHEALTH ALLIANCE INC
 Address: 1200 LINCOLN AVENUE PROSPECT PARK, NY 10001
 County: NEW YORK
 Country: United States of America
 Type: Supplier Organizations (Service, Supplies, Material and Equipment)
 Class: Private Profit (Small Business) Organizations

https://taggs.hhs.gov/Detail/RecipDetail?arg_RecipId=ZfeVER2uWwKlInTv6X4AxA%3D%3D

Company Information

Company Name: [ECOHEALTH ALLIANCE INC.](#)

Entity Type: FOREIGN NON-PROFIT CORPORATION

File Number: [F09000004818](#)

Filing State: Florida (FL)

Domestic State: Massachusetts (MA)

Filing Status: Inactive

Filing Date: December 4, 2009

Company Age: 11 Years, 7 Months

Principal Address:  [460 W. 34th St.](#)
[New York, NY 10001](#)

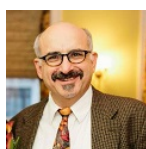
Mailing Address:  [460 West 34th Street](#)
[17th Floor](#)
[New York, NY 10001](#)

Source: Florida Department of State

Ecohealth Alliance Inc. is a **Florida Foreign Non-Profit Corporation** filed On **December 4, 2009**. The company's filing status is listed as Inactive and its File Number is F09000004818. The company's principal address is 460 W. 34th St., New York, NY 10001 and its mailing address is 460 West 34th Street 17th Floor, New York, NY 10001. The company has 5 principals on record. The principals are Peter Daszak from New York NY, Robert Hoquet from New York NY, Nells Lippert from New York NY, Ellen Shedlarz from New York NY, and Carol C Timmis from New York NY.

<https://www.bizapedia.com/fl/ecohealth-alliance-inc.html>

SAM HUSSEINI: PETER DASZAK'S ECOHEALTH ALLIANCE HAS HIDDEN ALMOST \$40 MILLION IN PENTAGON FUNDING AND MILITARIZED PANDEMIC SCIENCE



Sam Hussein is an Arab of Christian descent. Sam describes himself as a Jordanian-Palestinian writer and "political activist." He is the communications director of the Institute for Public Accuracy, a D.C.-based nonprofit group that promotes anti-Israel "progressive" experts as alternative sources for mainstream media reporters. He formerly worked at the American-Arab Anti-Discrimination Committee and at the media watch group Fairness and Accuracy in Reporting. He is funded by the Open Society Foundation headed by George Soros who collaborated with Nazis during WWII, however his reporting is accurate when it comes to Daszak.

This statement was written in the *New York Times* earlier this year by Peter Daszak. Daszak is the longtime president of the **EcoHealth Alliance**, a New York-based non-profit whose claimed focus is pandemic prevention. But the EcoHealth Alliance, it turns out, is at the very center of the COVID-19 pandemic in many ways. To depict the pandemic in such militarized terms is, for Daszak, a commonplace. In an **Oct. 7 online talk organized by Columbia University's School of International and Public Affairs**, Daszak presented a slide titled "Donald Rumsfeld's Prescient Speech:"

"There are known knowns; there are things we know that we know. There are known unknowns; that is to say, there are things that we know we don't know. But there are also unknown unknowns – there are things we don't know we don't know." (This Rumsfeld quote is in fact from a news conference.) In the subsequent online discussion, Daszak emphasized the parallels between his own crusade and Rumsfeld's, since, according to Daszak, the "potential for unknown attacks" is "the same for viruses." Daszak then proceeded with a not terribly subtle pitch for over a billion dollars. This money would support a fledgling virus hunting and surveillance project of his, the **Global Virome Project** – a "doable project" he assured watchers – given the cost of the pandemic to governments and various industries. Also on the video was Columbia University professor **Jeffrey Sachs**.



DASCHLE AND DASZAK: DASZAK IS REGISTERED DEMOCRAT

FORMER SENATOR THOMAS DASCHLE & PETER DASZAK DEMOCRATIC PARTY APPARATCHIKS

Sachs is a former special advisor to the UN, the former head of the Millennium Villages Project, and was recently appointed Chair of the newly-formed **EAT Lancet Commission on the pandemic**. In September 2021, Sachs' commission named Daszak to head up its committee on the pandemic's origins. Daszak is also on the **WHO's committee to investigate the pandemic's origin**. He is the only individual on both committees. These leadership positions are not the only reason why Peter Daszak is such a central figure in the COVID-19 pandemic, however. His appointment **dismayed many** of those who are aware that Daszak's EcoHealth Alliance funded bat coronavirus research, including virus collection, at the Wuhan Institute for Virology (WIV) and thus **could themselves be directly implicated in the outbreak**.

For his part, Daszak has **repeatedly dismissed** the notion that the pandemic **could have a lab origin**. In fact, a recent **FOIA by the transparency group U.S. Right To Know** revealed that Peter Daszak drafted an influential **multi-author letter** published on February 18 in the *Lancet*. That letter dismissed lab origin hypotheses as "conspiracy theory." Daszak was revealed to have orchestrated the letter such as to "avoid the appearance of a political statement."

Sachs for his part seemed surprised by Daszak's depiction of Rumsfeld but Daszak reassured him. "It's an awesome quote! And yes, it's Donald Rumsfeld, Jeff, and I know he's a Republican, but – what a genius!"

FOLLOWING THE ECOHEALTH ALLIANCE'S MONEY TRAIL TO THE PENTAGON

For much of this year, Daszak's EcoHealth Alliance garnered a great deal of sympathetic media coverage after its \$3.7 million five-year NIH grant was prematurely cut when the Trump administration learned that EcoHealth Alliance funded bat coronavirus research at the WIV. The temporary cut was widely **depicted in major media** as Trump undermining the EcoHealth Alliance's noble fight against pandemics. The termination was reversed by NIH in late August 2020, and even **upped to \$7.5 million**. But entirely overlooked amid the claims and counter-claims was that far more funding for the EcoHealth Alliance comes from the Pentagon than the NIH.

To be strictly fair to the media, Daszak's EcoHealth Alliance obscures its Pentagon funding. On its website EcoHealth Alliance states that "A copy of the EHA Grant Management Manual is available upon request to the EHA Chief Financial Officer at finance (at) ecohealthalliance.org". But an email to that address and numerous others, including Peter Daszak's, requesting that Manual, as well as other financial information, was not returned. Neither were repeated voicemails. Only **buried under their "Privacy Policy,"** under a section titled "EcoHealth Alliance Policy Regarding Conflict of Interest in Research," does the EcoHealth Alliance concede it is the "recipient of various grant awards from federal agencies including the National Institute of Health, the National Science Foundation, US Fish and Wildlife Service, and the US Agency for International Development and the Department of Defense."

Even this listing is deceptive. It obscures that its two largest funders are the Pentagon and the State Department (USAID); whereas the US Fish and Wildlife Service, which accounts for a minuscule \$74,487, comes before either.

Meticulous investigation of US government databases reveals that Pentagon funding for the EcoHealth Alliance from 2013 to 2020, including contracts, grants and subcontracts, was just under **\$39 million**. Most, \$34.6 million, was from the Defense Threat Reduction Agency (DTRA), which is a branch of the DOD which states it is tasked to **"counter and deter weapons of mass destruction and improvised threat networks."** Most of the remaining money to EHA was from USAID (State Dept.), comprising at least **\$64,700,000 (1)**. These two sources thus total over **\$103 million**. (See Fig).

SUMMARY

FEDERAL GRANTS & CONTRACTS

AGENCY	TOTAL
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DoD	\$38,949,941.00
HHS	\$13,023,168.00
NSF	\$2,590,418.00
USAID	\$2,499,147.00
DHS	\$2,272,813.00
DoC	\$1,241,933.00
USDA	\$646,701.00
DoI	\$267,062.00
GRAND TOTAL	\$61,491,183.00

Summary EHA Grants and Contracts. Note this figure doesn't count subcontracts so it undercounts USDA's contribution, see footnote (1) below (Credit: James Baratta and Mariamne Everett)

Another \$20 million came from Health and Human Services (\$13 million, which includes National Institutes of Health and Centers for Disease Control), National Science Foundation (\$2.6 million), Department of Homeland Security (\$2.3 million), Department of Commerce (\$1.2 million), Department of Agriculture (\$0.6 million), and Department of Interior (\$0.3 million). So, total US government funding for EHA to-date stands at \$123 million, approximately one third of which comes from the Pentagon directly. The full funding breakdown is [available here](#) and is summarized by year, source, and type, in a [spreadsheet format](#).

PDF versions of this spreadsheet are available to download. The summary is [here](#) and all Federal grants and contracts are [here](#).

MORE MILITARY CONNECTIONS

The military links of the EcoHealth Alliance are not limited to money and mindset. One noteworthy 'policy advisor' to the EcoHealth Alliance is David Franz. Franz is former commander of Fort Detrick, which is the principal US government biowarfare/biodefense facility. David Franz was part of UNSCOM which inspected Iraq for alleged bioweapons – what were constantly referred to as WMDs or Weapons of Mass Destruction by the US government and the media. Franz has been one of those eager to state, at least when discussing alleged Iraqi programs, that “in biology ... everything is dual use – the people, the facilities and the equipment.” (NPR, May 14, 2003; link no longer available). Just this year Franz wrote a piece with former *New York Times* journalist Judith Miller, whose stories of Iraqi WMDs did much to misinform the US public regarding the case for the 2003 invasion of Iraq. Their joint article, “[A Biosecurity Failure: America's key lab for fighting infectious disease has become a Pentagon backwater](#),” urges more funding for Fort Detrick. Miller and Franz are longtime associates. Miller co-wrote the book *Germs*, released amid [the 2001 false flag anthrax attacks](#), which repeatedly quotes Franz. Miller at the time received a hoax letter with a harmless white powder, increasing her prominence. Franz continued hyping the existence of Iraqi WMDs even after the invasion of Iraq. While she was still with the *Times*, Miller quoted him in a story “[US Analysts Link Iraq Labs To Germ Arms](#)” on May 21, 2003 pushing the theory that Iraq had mobile biological WMD units. (This theory [was debunked](#) by the British scientist Dr. David Kelly, who would die, [apparently by suicide](#), soon thereafter.¹

1. Samuel is hinting the Mossad took him out with no evidence to back up this assertion.

Four significant insights emerge from all this. First, although it is called the EcoHealth Alliance, Peter Daszak and his nonprofit work closely with the military. Second, the EcoHealth Alliance attempts to conceal these military connections. Third, through militaristic language and analogies Daszak and his colleagues promote what is often referred to as, and even then somewhat euphemistically, an ongoing agenda known as “[securitization](#)”. In this case it is the securitization of infectious diseases and [of global public health](#). That is, they argue that pandemics constitute a vast and existential threat. They minimize the very real risks associated with their work, and sell it as a billion dollar solution. The fourth insight is that Daszak himself, as the Godfather of the Global Virome Project, stands to benefit from the likely outlay of public funds. **Acknowledgments** Thanks to James Baratta and Mariamne Everett for researching the funding sources.

Footnote

1. The figure for EHA's USAID funding was obtained from the University of California at Davis, a major grantee of PREDICT funds, which EHA has been a major sub-grantee of Davis confirmed that EHA's funding from PREDICT totaled \$64,722,669 (PREDICT-1: 2009 to 2014: \$19,943,214; PREDICT-2: 2014 to present (2020) \$44,779,455)

This originally appeared in [Independent Science News](#).

Sam Hussein is a founder of [VotePact.org](#) – which helps break out of the two party bind. His latest personal writings are at <http://husseini.posthaven.com/> and tweets at <http://twitter.com/samhusseini>.

THE PREDICT PROGRAM WAS A CON JOB AND FAILURE: IT HAS BEEN ALLEGED THAT A LARGE PORTION OF THE GRANT MONEY WAS HIDDEN AWAY BY DASZAK FOR HIS OWN USE





TAIPEI (Taiwan News) — "A report by Independent Science News and a search of U.S. government databases revealed that EcoHealth Alliance received \$39 million in funding from the Pentagon from 2013 to 2020. Adding another \$64.7 million from USAID, the report found that Daszak's "non-profit organization" has raked in over US\$103 million from the U.S. government. Since 2014, Daszak's organization has funneled some of this U.S. government funding into the WIV to carry out research on bat coronaviruses. In the first phase of research, which took place from 2014 to 2019, Daszak coordinated with Shi Zhengli — also known as "Bat Woman" — at the WIV to investigate and catalog bat coronaviruses across China. EcoHealth Alliance received US\$3.7 million in funding from the NIH for this research, and 10 percent was channeled to the WIV, reported NPR. The second phase, which started in 2019, involved Gain-of-Function / Gain-of-Threat research on coronaviruses and chimeras in humanized mice from the lab of Ralph S. Baric of the University of North Carolina."

"A report by U.S. Right to Know alleges that emails released through freedom of information requests reveal that Daszak persuaded 26 prominent scientists to sign a statement published in *The Lancet* on Feb. 19 2020, claiming that any suggestions that COVID-19 was not of natural origin are "conspiracy theories." Four signatories of *The Lancet* statement are employed by EcoHealth Alliance. **Six scientists who signed the statement, including Daszak, now comprise half of The Lancet's panel investigating the origins of the virus.**"

"A prominent molecular biologist at Rutgers University claims that a member of the World Health Organization (W.H.O.) team investigating the origins of COVID-19 in Wuhan has a conflict of interest, due to his ties with the Wuhan lab at the center of the inquest. British zoologist and the president of EcoHealth Alliance Peter Daszak is the only individual to be part of both the W.H.O. and *The Lancet* teams investigating the origins of the Wuhan coronavirus pandemic. However, he has long-term professional and financial ties with the Wuhan Institute of Virology (WIV), which represents a conflict of interest. **Richard H. Ebright is the Board of Governors Professor of Chemistry and Chemical Biology at Rutgers University, and Laboratory Director at the Waksman Institute of Microbiology.** He told *Taiwan News* that Daszak is the contractor who funded the WIV's research on bat SARS-related coronaviruses, with subcontracts of \$200 million in USAID funding and \$7 million in NIH funding. Ebright said that Daszak is a collaborator on the WIV research for bat SARS-related coronaviruses. He lamented that the W.H.O. named Daszak as a member of its review team, and *The Lancet* named Daszak as the head of its review team. Ebright said this makes "it clear that W.H.O. and *Lancet* reviews cannot be considered credible investigations." In addition to the funding EcoHealth Alliance receives from USAID, NIH, and other agencies, which it funnels into the WIV, Ebright stated the firm received US\$30 million from the US Department of Defense. When asked whether Daszak had been involved in the controversial gain-of-function / gain-of threat experiments on bat coronaviruses at the WIV, Ebright said: **"Daszak has been a contractor, a collaborator, and a co-author on work at the WIV on construction and analysis of novel chimeric coronaviruses."**

"Furthermore, Daszak in 2015 co-authored an article in the journal *Nature* titled, "Spillover and pandemic properties of zoonotic viruses with high host plasticity," in which he stated that zoonotic virus spillover from wildlife was "most frequent" in a number of settings and occupations, including "laboratory workers." He also warned that laboratories are one of the most dangerous settings for major spillover events. "Among all high risk interfaces and hosts, only viruses transmitted to humans by contact with wild animals in the wildlife trade and in laboratories ... were more likely to have broader geographic reach," Daszak said. Daszak's colleague, SHI ZHENGLI, in 2010 published a paper describing a scenario in which infected rodents led to a deadly virus being leaked from a Chinese lab. The paper, titled, "Hantavirus outbreak associated with laboratory rats in Yunnan, China," detailed an outbreak of hantavirus hemorrhagic fever with renal syndrome (HFRS) at a college in Kunming as the result of a lab leak in 2003."

Since the start of the pandemic, both Daszak and Shi have denied that a lab leak occurred at the WIV. However, over a year since the outbreak, Shi has yet to provide independent investigators with access to the WIV's database and laboratory records. Daszak has yet to respond to a request to comment on allegations that he has a conflict of interest in the W.H.O. and *The Lancet* investigations. The WIV has also yet to reply to questions about their experiments in 2019.

<https://www.taiwannews.com.tw/en/news/4119101>

CHAPTER 30

ECOHEALTH ALLIANCE STAFF AND DUPES

[Nancye Green](#) founded Donovan/Green with Michael Donovan, designing and producing experiences in multiple media for clients as diverse as American Museum of Natural History, California Science Center, Liberty Science Center, IBM, GM, P&G, President Ronald Reagan, Sony and American Girl. Parsons School of Design - The New School Degree Name BFA Field Of Study Environmental Valedictorian of Parsons Graduating Class Tulane University Degree Name BA Field Of Study Political Science. Also see [Nancye Green](#)

David Amburgey. Hand Baldachin & Amburgey LLP

Dr. Amy Attas [Civil Court, City of New York, Claire RATUSCH, Plaintiff, v. Dr. Amy ATTAS d/b/a Center for Veterinary Care, Defendant. Decided: March 26, 2004](#)

Dr. Frederick Baum Leading the development of a small animal veterinary hospital in rural Vermont towards a progressive state of the art practice network by incorporating advanced veterinary services, IT, human resources, customer service, marketing, strategy, and customer service. Board of Directors, EcoHealth Alliance. Board of Directors to the VIN Foundation in Davis California. Charitable arm of the Veterinarian Information Network (VIN) supporting and uniting over 50,000 veterinarians in transition across the country and around the world. <https://thearlingtonvet.com/team>

[Gerard Caddick](#) Founded in 1990, The International Ecotourism Society has been on the forefront of the development of Ecotourism, providing guidelines and standards, training, technical assistance, and educational resources.

[Dr. Rita Colwell](#) Dr. Rita R. Colwell, Ph.D., is a microbiologist and marine scientist. She is active in national and international research and teaching. Much of her research has focused on the effects of bacteria on the Chesapeake Bay, in deep seas, and in recreational waters.

[Dr. Marianne De Backer](#) Marianne De Backer, PhD, MBA Member of the Bayer AG Pharmaceuticals Executive Committee & Executive Vice President and Head of Strategy, Business Development & Licensing Dr. Marianne De Backer has been a strategist, scientist, business leader, deal maker and corporate investor in the healthcare industry for more than two decades. Also see: [**MARIANNE DE BACKER**](#)

[Oliver Engert](#) Since joining McKinsey in 1993, Oliver has worked with top executives in all sectors, pursuing strategic growth and operational performance. He has developed deep expertise in helping pharmaceutical and medical-device companies pursue performance improvement against a backdrop of intense competitive pressure.

[Margery Fischbein](#) Prior to joining Cassel Salpeter, Margery was Head of Healthcare Investment Banking for Seaport Global and FBR & Co., and Head of East Coast Biotechnology Investment Banking for JMP Securities. Margery held senior executive positions with Human Genome Sciences and ImClone Systems, who were leaders in their field until being acquired by GlaxoSmithKline and Eli Lilly and Company, respectively. Margery started her investment banking career at Lehman Brothers (where she rose to Senior Vice President) and was then a Managing Director of Investment Banking at JP Morgan Chase and Citigroup.

[Nancy Griffin](#) Bayer Pharmaceuticals Total Duration 9 yrs Title Alliance Management Dates Employed 1998 – 2007 Employment Duration 9 yrs Title Director, Operations Dates Employed 2000 – 2002

[Holly Hegener](#) Chief Operating Officer Dates Employed May 2017 – Jan 2020 Trewstar is a search firm that focuses on placing highly-qualified and outstanding women on corporate boards. Over the past three years, we have placed dozens of women on corporate boards representing a diverse set of industries and locations throughout the US. While most of our clients are Fortune 500 companies, we have also done placements for small and mid-cap companies and pre-IPO companies.

[Bob Hogue](#) Bob has a BA from Harvard College, an LLB from New York University Law School, and an MBA and a Certificate in Conservation Biology from Columbia University.

[Dr. Patricia Verduin](#) Dr. Patricia Verduin is the Chief Technology Officer for Colgate Palmolive Company where she provides leadership for product innovation, clinical science and long-term research and development. Prior to this role, Dr. Verduin's career spanned technical leadership positions in the food industry including ConAgra Foods where she was Senior Vice President of Product Quality and Development as well as Nabisco where she held various product development and innovation leadership positions. In addition to industry, Dr. Verduin was the Chief Scientific Officer at the Grocery Manufacturers/Food Products Association. She also holds several patents from her research. Dr. Verduin received her B.S. degree from the University of Delaware and her M.B.A. in Finance from Farleigh Dickinson University. She received her Ph.D. in Food Science from Rutgers University.

[Dr. James Hughes M. D.](#) is Professor of Medicine and Public Health at Emory University and Co-Director of the Emory Antibiotic Resistance Center. Prior to joining Emory, he worked for the Centers for Disease Control and Prevention (CDC), initially as an Epidemic Intelligence Service (EIS) officer and ultimately as Director of the National Center for Infectious Diseases from 1992-2005. Dr. Hughes received his M.D. degree from Stanford University and trained in internal medicine at the University of Washington, infectious diseases at the University of Virginia, and preventive medicine at CDC. He is a member of the National Academy of Medicine (NAM), Vice Chair of the NAM Forum on Microbial Threats, and a past president of the Infectious Diseases Society of America (IDSA).

[Bob Kuperman](#) Bob Kuperman, has a storied career with more than 40 years of experience creating some of the most historically famous and brand-effective advertising in the U.S. Mr. Kuperman began his career in 1963 at Doyle Dane Bernbach as an Art Director, working on much of their landmark, award-winning advertising, and during his three years as head of the Volkswagen group, created such classics as "1949 Auto Show." A collection of his Volkswagen ads hangs in the Smithsonian Institution.

[Margaret Loeb](#) **McKinsey & Company** Total Duration 32 yrs 10 mos Title Senior Advisor Dates Employed Aug 2012 – Present Employment Duration 8 yrs 10 mos Title Director of Client Communications Dates Employed Aug 1988 – Aug 2012 Morgan Stanley Dean Witter CEO Speech Writer Feb 1987 – July 1988 The Wall Street Journal Staff Reporter; Editor The Wall Street Journal Dates Employed Nov 1981 – Feb 1987 Tulane University Medill School of Journalism, Northwestern University New School for Social Research. Also see: [**MARGARET MUNZER LOEB**](#)

[Dr. Thomas Lovejoy](#) Thomas E. Lovejoy was elected University Professor at George Mason in March 2010. He previously held the Biodiversity Chair at the Heinz Center for Science, Economics and the Environment and was President from 2002-2008. An ecologist who has worked in the Brazilian Amazon since 1965, he works on the interface of science and environmental policy. He received his B.S. and Ph.D. (Biology) from Yale University. Stemming population growth is a cheap way to limit climate change by Thomas Lovejoy [**EcoFascist**](#)

[Joel A. Maizel](#) Director in Prime Services at Barclays, based in New York. Mr. Maizel is responsible for leading Barclays Capital Solutions efforts for quantitative hedge funds and liquid strategies investors. Maizel holds a Bachelor of Arts degree from the University of Arizona, and a Juris Doctor degree from the Southern Methodist University, Dedman School of Law.

[David McIntyre](#) McIntyre is an attorney with over 25 years of experience, including most recently with Johnson & Johnson where he has served as in-house counsel for over 17 years. He received his JD from Fordham University School of Law, and a BS degree in Biology from Cornell University.

[Lori Michelin](#) Ms. Michelin comes from the Colgate-Palmolive Company, where she led their global sustainability initiatives as the Vice-President of Sustainability and Environmental, Health, and Safety. She received her Master of Science in Civil Engineering from Villanova University and holds a degree in Civil Engineering from Pennsylvania State University. Also see: [**Lori Michelin**](#)

[Ann Moore](#) Ann Moore comes to the organization with 15 years experience as a seasoned events and public relations professional with a diverse background in corporate sales, vendor management, production and talent management. Ms.

Moore is currently a special events consultant and continues to provide expertise to high profile clients. Previously, Ms. Moore has produced events for such organizations as the New York City Ballet, The Michael J. Fox Foundation, Jazz at Lincoln Center and the Whitney Museum. Her expertise lies in executing large-scale fundraising galas.

[Mark O'Donnell](#) James McGreevey is best known as the self-described "gay American" who, threatened with blackmail by a lover whom he'd placed on the state payroll, resigned as New Jersey's governor in 2004. His partner, Mark O'Donnell, is an Australian financier with a taste for modern art and adventure travel. Also see: [Mark O'Donnell](#)

[Sheila Patel](#) Sheila Patel, chairman of Goldman Sachs Group Inc.'s asset-management unit, is leaving the \$1.8 trillion division after almost two decades at the firm.

[Ellen Shedlarz](#) Shedlarz joins Hill & Knowlton from Mercer Delta where she served as chief administrator officer and was responsible for building a human resource function, as well as creating key people management processes. Prior to Mercer Delta, Shedlarz was an administrative partner of **McKinsey & Company**, responsible for the administration and operations of six locations.

[Lisa Silvershein](#) Ms. Silvershein holds a Bachelor's degree in Psychology from Dickinson College and a Master's in Human Resources Management from Upsala College.

[Carlota Vollhardt](#) Carlota has over 25 years of international experience in leadership, consulting, and academic positions based in the US, UK and Germany, and has consulted or led projects in other European countries and in Japan, China and Korea. Prior to launching EKI she held positions of increasing responsibility at Pfizer Inc. in global talent, organizational development, and knowledge management. Also see: [Carlota Vollhardt](#)

[Lucy Stitzer](#) Lucy Stitzer chairs Waycrosse, the investment company of the Cargill and MacMillan families, one of the 10 richest clans in America. Stitzer owns an estimated 3% stake in Cargill, the largest food company in the world. She's one of four billionaire sisters who inherited stakes in the company from their father W. Duncan MacMillan, who died in 2006. Her great-great-grandfather, W.W. Cargill, founded the business as a single grain warehouse on the end of an Iowa railroad line in 1865. The family still owns roughly 90% of Cargill, which did \$114.6 billion in 2020 sales across food, agriculture, financial and industrial divisions.

[Pamela Thye](#) Socialite do-gooder dupe.

Ann Moore and Dr. Patricia Verduin

[ECO SCIENTISTS](#)

[ECO BOARD OF DIRECTORS](#)

SOME OF USAID/CIA ECO-HEALTH PREDICT CREW

This Operation is built around the PREDICT program that failed the American people. The scientists involved in EcoHealth are wildlife / human interface scholars and have no idea of what went on in WIV.



Dr. Alice Latinne Research Scientist As a research scientist at EcoHealth Alliance, Dr. Alice Latinne aims at better understanding the dynamics of pathogens within and among wildlife populations, livestock, and humans, with a focus on projects in Asia. Alice studies the evolutionary dynamics of host-pathogen interactions, and their co-evolution at the phylogenetic and phylogeographic scale, in order to assess the risk of zoonotic pathogens emergence at high-risk human-wildlife interfaces. Alice's work aims to explain patterns and likelihood of pathogen sharing among species, and to determine how the host phylogenetic and phylogeographic structure affects pathogen distribution and cross-species transmission. Alice is currently involved with our work on Nipah virus and host dynamics in S. Asia and **assessing the risk of bat Coronavirus emergence in live animal markets of southern China**. Trained as an evolutionary biologist, Alice earned her M.Sc. in Animal Biology and her Ph.D. in Molecular Biology at the University of Liège in Belgium. Her Ph.D. dissertation aimed at exploring the diversity and evolutionary history of murid rodents in limestone karsts of Thailand. During her doctoral research, Alice has spent a long time trapping rodents and small mammals in Southeast Asia before analysing the collected samples in genetics laboratory. Prior to her current position at EcoHealth Alliance, Alice was a Marie Curie COFUND fellow and she conducted postdoctoral research at the Institut des Sciences de l'Evolution in Montpellier (ISEM) and at the Kasetsart University in Thailand. Her research goals were directed toward understanding the evolution of murid rodents and their associated parasites and pathogens in Southeast Asia.



Dr. Kendra Phelps applies her keen interest in the ways that humans alter our own environment in her work creating bat surveillance networks in Western Asia. Through establishing a network of bat disease ecologists in the region which has previously been poorly studied, Kendra aims to expand our knowledge of the diseases bats can potentially spread to humans, and the ways in which humans can shift our own behaviors to prevent such disease spillovers. Dr. Phelps earned a BS from Auburn University and a Ph.D in Zoology from Texas Tech University.¹ She also worked in the Philippines as a Fulbright Fellow, there she studied cave-dwelling bats' responses to cave disturbance and the interactions people living near those caves had with the bat populations. Before joining EcoHealth Alliance, Dr. Phelps worked as a lecturer and research associate at her alma mater, Texas Tech.

A group of Texas Universities was suspected of having undisclosed ties to the Chinese.



Dr. Anne Laudisoit is an eco-epidemiologist and wildlife biologist who, through her interest in the interface between human, animal, and environmental health, became a One Health disease ecologist. Dr. Laudisoit holds a joint Ph. D from the University of Antwerp and Liège working on plague epidemiology in Tanzania. Dr. Laudisoit has spent extensive time in Africa; she has spent the last several years in the Democratic Republic of Congo studying neglected tropical diseases like onchocerciasis-associated epilepsy, emerging zoonotic diseases like monkeypox, Rickettsia, and Bartonella, and teaching at the University of Kisangani. She now

works with EcoHealth Alliance on the PREDICT program, aiming to predict future viral epidemics globally.

EcoHealth Alliance works at the leading edge of this field by building local capabilities and testing high-risk wildlife in Bangladesh, Côte d'Ivoire, Republic of Congo, China, Egypt, India, Indonesia, Jordan, Liberia, Malaysia, and Thailand. After scientists collect swabs or small amounts of blood, they analyze the samples in the lab to look for evidence of disease. The findings are catalogued in a database, that mathematical experts use to create predictive maps of potential disease outbreaks. This approach not only allows researchers to find new diseases, but also helps communities prepare for and respond to the threat of an outbreak.



Tom Hughes Senior Scientist As Malaysian Project Coordinator at EcoHealth Alliance, Tom Hughes coordinates all of our sampling, testing, capacity building and training efforts in Malaysia. Tom's responsibilities include setting up and running the Study of Zoonotic Infections among Persons Exposed to Wild Animals, a collaborative research project with the Malaysian Government, as well as being the *PREDICT country coordinator for the USAID Emerging Pandemic Threats program and Deputy Chief of Party for the USAID Infectious Disease Emergence and Economics of Altered landscapes (IDEEAL) Project*. Tom began working with EcoHealth Alliance in June 2005 on the Nipah virus research project in Malaysia. In 2007, he took on the new role of coordinating the Study of Zoonotic Infections among Persons Exposed to Wild Animals in Malaysia, to determine if close contact with wild animals results in the transfer of zoonotic diseases. In 2010, Tom became the PREDICT Malaysia country coordinator for USAID's Emerging Pandemic Threats program. The aim of this research is to create an early warning system for potential zoonotic disease spillover into livestock and humans. Tom is working closely with partners from the Ministry of Health, the Department of Wildlife and National Parks, the Department of Veterinary Services, Sabah Wildlife Department and local universities to develop personnel and laboratory capacity and establish sustainable disease surveillance systems.

Executives Listed on Filing

Total Salary includes financial earnings, benefits, and all related organization earnings listed on tax filing

Name	Title	Hours Per Week	Total Salary
Peter Daszak Phd	PRESIDENT	40	\$354,065
William Karesh	EXECUTIVE VICE PRESIDENT	40	\$274,730
Armine Arustamyan	CHIEF FINANCIAL OFFICER	40	\$186,603
Leilani Francisco	SENIOR SCIENTIST	40	\$167,417
Kevin Olival	VICE PRESIDENT FOR RESEARCH	40	\$151,650
Jonathan Epstein	VICE PRESIDENT	40	\$146,587
Evelyn Luciano	SR. FEDERAL GRANTS DIRECTOR	40	\$139,488
Ellen Carlin	HEALTH AND POLICY SPECIALIST	40	\$137,150
Aleksei Chmura	CHIEF OF STAFF	40	\$131,441
Anthony Ramos	SENIOR DIRECTOR OF MARKETING	40	\$129,305
Mark O'Donnell	DIRECTOR	3	\$0
Lisa Silvershein	DIRECTOR	3	\$0
Pamela Thye	DIRECTOR	3	\$0
Lucy Stitzer	DIRECTOR	3	\$0
Sheila Patel	DIRECTOR	3	\$0
Marianne De Backer	DIRECTOR	3	\$0
David McIntyre	DIRECTOR	3	\$0
Joel Maizel	DIRECTOR	3	\$0
James Hughes	DIRECTOR	3	\$0
Margaret Loeb	DIRECTOR	3	\$0
Bob Kuperman	DIRECTOR	3	\$0
Peter Kaufman	DIRECTOR	3	\$0
Gerard Caddick	DIRECTOR	3	\$0
Rita Colwell	DIRECTOR	3	\$0
Holly Hegener	DIRECTOR	3	\$0
Fredrick Baum	DIRECTOR	3	\$0
Margery Fishbein	DIRECTOR	3	\$0
Amy Attas	DIRECTOR	3	\$0
Davud Amburgey	DIRECTOR	3	\$0
Robert Hogue	TREASURER	3	\$0
Lori Michelin	VICE CHAIR	3	\$0
Carlota Vollhardt	SECRETARY	3	\$0
Nancye Green	CHAIR	3	\$0

PAID EMPLOYEES OF ECO-HEALTH ALLIANCE



Dr. William B. Karesh is the Executive Vice President for Health and Policy at EcoHealth Alliance. He serves as the president of the World Animal Health Organization (OIE) Working Group on Wildlife Diseases and also chairs the International Union for the Conservation of Nature (IUCN) Wildlife Health Specialist Group, a network of wildlife and health experts around the world. Dr. Karesh also serves on the World Health Organization's (W.H.O.) International Health Regulations Roster of Experts focused on the human-animal interface and wildlife health. Currently, Dr. Karesh is the EPT Partner Liaison for the USAID Emerging Pandemic Threats PREDICT-2 program, a >\$120 million effort focused on predicting and preventing pandemic diseases. He is a Life Member of the Council on Foreign Relations.



Armine Arustamyan California Intercontinental University Degree Name Doctoral Field Of Study Business Administration Dates attended or expected graduation 2010 – 2014 Activities and



Societies: Global Business Leadership American University of Armenia Degree Name Master's Degree Field Of Study System Management and Industrial Engineering Dates attended or expected graduation 1995 – 1997 Yerevan State University Degree Name Master Field Of Study Science in Physics Dates attended or expected graduation 1987 – 1992



Leilani Francisco PhD MA PMP The Johns Hopkins University Degree Name Ph.D. Field Of Study International Public Health University of Maryland College Park Degree Name B.A. Field Of Study Sociocultural Anthropology University of South Florida Degree Name M.A. Field Of Study Applied Medical Anthropology



Dr. Epstein received a PhD in Disease Ecology from Kingston University, London and his DVM and MPH from Tufts University. A veterinarian and disease ecologist, Dr. Jonathan Epstein is the Vice President for Science and Outreach at EcoHealth Alliance. His research focuses on the ecology of emerging zoonotic viruses such as Nipah and Ebola virus, along with SARS, Middle East Respiratory Syndrome (MERS), and others that have emerged within Asia and Africa.



Evelyn Luciano Rollins College Degree Name Master of Arts (MA) Field Of Study Human Resources Management and Services Certificate Dates attended or expected graduation 2003 – 2003 Rollins College Degree Name Master of Arts (MA) Field Of Study Counseling Psychology dates attended or expected graduation 1995 – 1999 Community Mental Health and School Counseling Catholic University of Puerto Rico Degree Name BSN Field Of Study Bachelor of Science In Nursing Grade BSN Dates attended or expected graduation 1975 – 1979



Dr. Ellen Carlin DVM is Assistant Research Professor at the Center for Global Health Science and Security, with a primary faculty appointment within the Department of Microbiology and Immunology. Her research interests are in the epidemiology of emerging infections. She studies incidence and transmission dynamics of zoonotic pathogens, focusing on the interfaces among people, animals, and the environments in which they live. She was Senior Professional Staff with the U.S. House of Representatives Committee on Homeland Security (Peter T. King, NY), where for more than five years she handled medical preparedness, biodefense, and science and technology policy. At Georgetown, Ellen is also the director of the Global Infectious Disease graduate program at the Graduate School of Arts and Sciences.



Aleksei Chmura: Experienced Chief Of Staff with a demonstrated history of working in the non-profit organization management industry. Skilled in Nonprofit Organizations, Environmental Science, Research, Community Outreach, and Budgeting. Strong administrative professional with a Doctor of Philosophy - PhD focused in Biology/Biological Sciences, General from Kingston University. Kingston University is ranked 581 in QS World University Rankings by TopUniversities and enjoys a poor reputation.



Anthony Ramos: Former Senior Director Marketing and Development at EcoHealth Alliance Former Director of Marketing at Schneider Associates Studied Classic Culinary Arts at The French Culinary Institute Studied International relations at Boston University Lives in Lake, Michigan.

CHAPTER 31

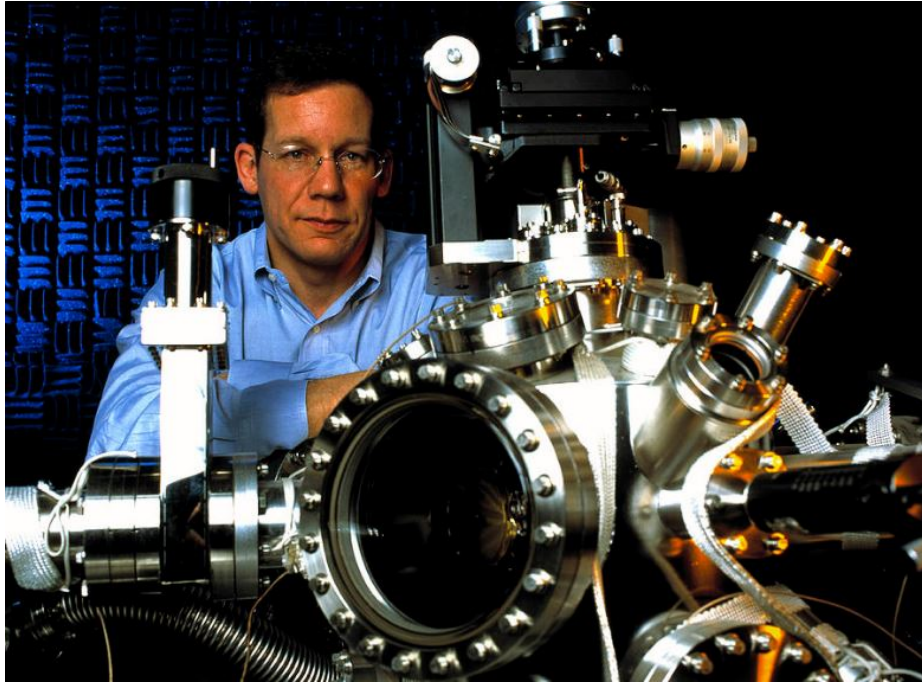
DASZAK IS CO-OPTED BY THE CHINESE AND BECOMES A CHINESE AGENT-OF-INFLUENCE



DASZAK: I'm in charge of in the organization in China... So the point is to establish capabilities in other countries not just take specimens from them and bring them back... that's the strategy and you know this the old adage that if you teach people how to do it, give them the tools then you've really made a difference. The money always dries up and this is something we've seen in the nonprofit world. You get great funding for five years from the foundation they always shift priorities because that's what emerged they closed them down. We have our staff in countries. We have sub contracts through local universities or agencies in-country and we have contracts to do work and it's all collaborative science so people love to interact on collaborative science. You know what I found especially in places like China where increasingly there's a paranoia around collaboration. Science collaboration is open and transparent because of the nature of what you're trying to do you're trying to discover stuff quickly, understand what it means, publish it in high-impact journal, and that drives openness and transparency and that's been great for us around the world it's also great for the U.S. and that's we really need to push that agenda. I think publishing is a very interesting mechanism you have to publish that's the argument




we use.

HOW MUCH CHINESE MONEY HAS DASZAK HIDDEN AWAY?



A Boston federal jury found Dr. Charles Lieber guilty of two counts of making false statements to the U.S. government about whether he participated in Thousand Talents Plan, a program designed by the Chinese government to attract foreign-educated scientists to China. They also found him guilty of failing to declare income earned in China and failing to report a Chinese bank account. Dr. Lieber's conviction is a victory for the [China Initiative](#) - an effort launched in 2018, under the Trump administration, to root out scientists suspected of sharing sensitive information with China. Dr. Lieber launched a joint venture in 2011 with the Wuhan University of Technology. A three-year contract emailed to Dr. Lieber in 2012, and displayed to the jury by prosecutors, identified him as a "One Thousand Talent High Level Foreign Expert," entitling him to \$50,000 a month, plus about \$150,000 in living expenses and more than \$1.5 million for a laboratory, which they called the WUT-Harvard Joint Nano Key Laboratory. At first, he denied receiving income from the Wuhan university or participating in the Chinese recruitment program. Then the agents produced a series of documents, including contracts from 2011 and 2012, and Dr. Lieber examined them, remarking at one point, "I should pay more attention to what I'm signing." He went on to offer detail about his financial arrangements with the Wuhan university: A portion of his salary was deposited in a Chinese bank account and the remainder — an amount he estimated as between \$50,000 and \$100,000 — was paid in \$100 bills, which he carried home in his luggage. [NYT](#)

CHI COM PROPAGANDA QUOTES PETER DASZAK WHO HAS BEEN "CO-OPERATING WITH THE WIV FOR 15 YEARS"

 **People's Daily, China** 
China state-controlled media · May 9, 2020 · 

#FactSheet on #COVID19: Was the coronavirus the result of a lab accident at the Wuhan Institute of Virology?

Established in 1956 and located just 30 kilometers from downtown Wuhan, the Wuhan Institute of Virology is the top virology research institute in China and home to Asia's highest-level biosafety lab. The biosafety level-4 lab can handle the world's deadliest pathogens.

Before accepting the first batch of test samples from COVID-19 patients on December 30, 2019, the institute's labs did not have the novel coronavirus and no one at the institute has contracted COVID-19 to this day.

"It is impossible for the virus to leak from such a high-security laboratory," said Yuan Zhiming, a researcher at the Wuhan Institute of Virology in an interview with CGTN on April 18.

The claim that the novel coronavirus escaped from the laboratory is pure nonsense, said Peter Daszak, chairperson of EcoHealth Alliance, a New York-based non-profit organization, who has been cooperating with the Wuhan Institute of Virology for 15 years.

There is no virus cultivation related to the new coronavirus in the laboratories of the Wuhan Institute of Virology, so the so-called "laboratory leak theory" is impossible, said Daszak, who is responsible for studying emerging infectious diseases worldwide.

You can read more here:
https://www.democracynow.org/.../4/16/peter_daszak_coronavirus
<https://news.cgtn.com/.../CGTN-Exclusive-Where-was.../index.html>

Daszak is a double agent who CIA thought was working for them but had been rolled over by the Chinese

Communist Party because his father was a Nazi War Criminal, a death camp executioner, who taught him to respect authoritarian governments. Daszak became a W.H.O. & Lancet inspector. A good place to be to cover-up for the Chinese and himself after he funneled money to the WIV and to the Bat Lady experiments which resulted in COVID-19 being created. And there is the question of how much money was siphoned off by Daszak?

Daszak: "I've seen incredible efforts from everything from [religious sect] Falun Gong to the [Chinese dissident] Miles Guo camp, Steve Bannon's group pushing the conspiracy theories around China. It's useful to them. They're funding it and pushing it and science has been to some extent caught up in that to other instances absolutely crushed by it. We've not had access to work in China on the origins for the last 12 months, which is ironic because we could have been on the ground there working with our Chinese colleagues and by now we could have found some really important answers. The rhetoric has held that up. We need that communication [with the Chinese] in an outbreak to learn from them how they control it so we can control it better. It's sad to say, but it will probably cost lives. By sort of narrow-mindedly focusing in on ourselves, or on labs, or on certain cultural politics, we miss the real enemy."

Daszak was a prime target of Chinese intelligence recruitment as he was already in bed with the CCP via EcoHealth. He parrots the Party Line. But he also was co-opted by the CIA until Trump cut his funds off. ECOHEALTH is a think tank put together by the AID CIA LITE that was supposed to protect America from Pandemics by keeping an eye on bats. But ECOHEALTH began to subsidize Gain-of-Function / Gain-of-Threat experiments at WIV and a recombinant virus leaked from the lab into the streets of Wuhan then into the market and out again. Was it coincidence that SARS-CoV2 started close to WIV? Just how close the Chinese won't say as they refuse to give out the address of patient zero.

STATE DEPARTMENT REPORT BASED ON CIA INTELL REVEALS DASZAK WAS INVOLVED IN CHINESE MILITARY PROJECTS [SEE REPORT](#)

"THE UNITED STATES AND OTHER DONORS WHO FUNDED OR COLLABORATED ON CIVILIAN RESEARCH AT THE WIV HAVE A RIGHT AND OBLIGATION TO DETERMINE WHETHER ANY OF OUR RESEARCH FUNDING WAS DIVERTED TO SECRET CHINESE MILITARY PROJECTS AT THE WIV." [US EMBASSY FACT SHEET](#)

The U.S. government has reason to believe that several researchers inside the WIV became sick in autumn 2019, before the first identified case of the outbreak, with symptoms consistent with both COVID-19 and common seasonal illnesses. This raises questions about the credibility of WIV senior Researcher Shi Zhengli's public claim that there was "zero infection" among the WIV's staff and students of SARS-CoV-2 or SARS-related viruses. Accidental infections in labs have caused several previous virus outbreaks in China and elsewhere, including a 2004 SARS outbreak in Beijing that infected nine people, killing one. The CCP has prevented independent journalists, investigators, and global health authorities from interviewing researchers at the WIV, including those who were ill in the fall of 2019. Any credible inquiry into the origin of the virus must include interviews with these researchers and a full accounting of their previously unreported illness. Starting in at least 2016 – and with no indication of a stop prior to the COVID-19 outbreak – WIV researchers conducted experiments involving RaTG13, the bat coronavirus identified by the WIV in January 2020 as its closest sample to SARS-CoV-2 (96.2% similar). The WIV became a focal point for international coronavirus research after the 2003 SARS outbreak and has since studied animals including mice, bats, and pangolins. The WIV has a published record of conducting "gain-of-function" research to engineer chimeric viruses. But the WIV has not been transparent or consistent about its record of studying viruses most similar to the COVID-19 virus, including "RaTG13," which it sampled from a cave in Yunnan Province in 2013 after several miners died of SARS-like illness. W.H.O. investigators must have access to the records of the WIV's work on bat and other coronaviruses before the COVID-19 outbreak. As part of a thorough inquiry, they must have a full accounting of why the WIV altered and then removed online records of its work with RaTG13 and other viruses.

Secrecy and non-disclosure are standard practice for Beijing. For many years the United States has publicly raised concerns about China's past biological weapons work, which Beijing has neither documented nor demonstrably eliminated, despite its clear obligations under the Biological Weapons Convention. Today's revelations just scratch the surface of what is still hidden about COVID-19's origin in China. Any credible investigation into the origin of COVID-19 demands complete, transparent access to the research labs in Wuhan, including their facilities, samples, personnel, and records. As the world continues to battle this pandemic – and as W.H.O. investigators begin their work, after more than a year of delays – the virus's origin remains uncertain. The United States will continue to do everything it can to support a credible and thorough investigation, including by continuing to demand transparency on the part of Chinese authorities. Despite the WIV presenting itself as a civilian institution, **the United States has determined that the WIV has collaborated on publications and secret projects with China's military. The WIV has engaged in classified research, including laboratory animal experiments, on behalf of the Chinese military since at least 2017. The United States and other donors who funded or collaborated on civilian research at the WIV have a right and obligation to determine whether any of our research funding was diverted to secret Chinese military projects at the WIV.**

ENSURING A TRANSPARENT, THOROUGH INVESTIGATION OF COVID-19'S ORIGIN PRESS STATEMENT MICHAEL R. POMPEO, SECRETARY OF STATE JANUARY 15, 2021

The United States has repeatedly called for a transparent and thorough investigation into the origin of COVID-19. Understanding the origin of this pandemic is essential for global public health, economic recovery, and international security. To assist the vital work of the World Health Organization (W.H.O.) investigative team that arrived in China this week, the United States government is today sharing new information concerning the activities inside China's government laboratories in 2019. In particular, we urge the W.H.O. to press the government of China to address the following: Illnesses at the Wuhan Institute of Virology (WIV): The United States government has reason to believe that several researchers inside the WIV became sick in autumn 2019, before the first identified case of the

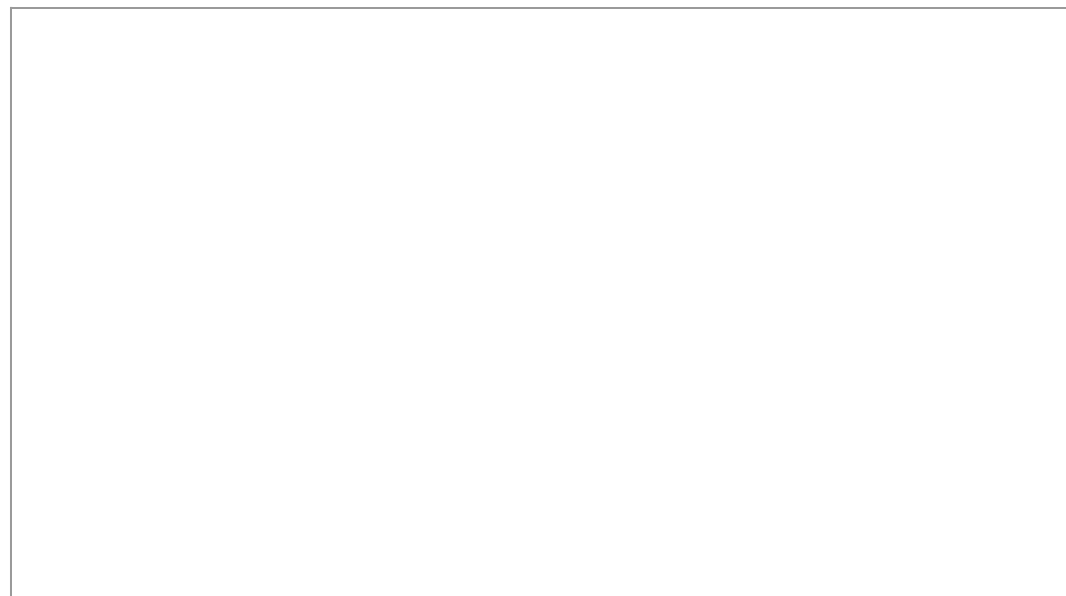
outbreak, with symptoms consistent with both COVID-19 and common seasonal illnesses. This raises questions about the credibility of WIV senior researcher Shi Zhengli's public claim that there was "zero infection" among the WIV's staff and students of SARS-CoV-2 or SARS-related viruses. WIV Research on "RaTG13" and "gain-of-function": Starting in at least 2016, WIV researchers studied RaTG13, the bat coronavirus identified by the WIV in January 2020 as its closest sample to SARS-CoV-2 (96.2% similar). Since the outbreak, the WIV has not been transparent nor consistent about its work with RaTG13 or other similar viruses, including possible "gain-of-function" experiments to enhance transmissibility or lethality. Secret WIV Links to Military Research: Despite the WIV presenting itself as a civilian institution, the WIV has collaborated on publications and secret projects with China's military. The WIV has engaged in classified research, including laboratory animal experiments, on behalf of the Chinese military since at least 2017. The COVID-19 pandemic was avoidable. Any responsible country would have invited world health investigators to Wuhan within days of an outbreak. China instead refused offers of help – including from the United States – and punished brave Chinese doctors, scientists, and journalists who tried to alert the world to the dangers of the virus. Beijing continues today to withhold vital information that scientists need to protect the world from this deadly virus, and the next one. The United States reiterates the importance of unfettered access to virus samples, lab records and personnel, eyewitnesses, and whistleblowers to ensure the credibility of the W.H.O.'s final report. Until the CCP allows a full and thorough accounting of what happened in Wuhan, it is only a matter of time until China births another pandemic and inflicts it on the Chinese people, and the world.

<https://2017-2021.state.gov/ensuring-a-transparent-thorough-investigation-of-covid-19s-origin/index.html>



DASZAK WORKED IN CHINA FOR 15 YEARS - RECRUITED BY CHINESE INTELLIGENCE

<https://www.nytimes.com/2020/01/28/science/bats-coronavirus-Wuhan.html>



Baric taught SHI ZHENGLI all she knows about virus creation at the University of North Carolina. Collwell is focused on oceans. Saif is a vet. Hume Field and rest work for the bio-war criminal, Daszak!

Dr. Peter Daszak, president of EcoHealth Alliance, who has been working in China for 15 years studying diseases that jump from animals to people, said, "We don't know the source yet, but there's pretty strong evidence that this is a bat origin coronavirus." He said, "It's probably going to be the Chinese horseshoe bat," a common species that weighs up to an ounce.

DASZAK BLAMES UNITED STATES FEDERAL GOVERNMENT FOR MONKEY POX

But zoonoses fall into a gray area, and the 2003 monkeypox outbreak in the Midwest is a perfect example of what can go wrong, said Peter Daszak, director of the Consortium for Conservation Medicine at the Wildlife Trust, a group specializing in human-animal diseases. The disease, related to smallpox but less deadly, arrived in a shipment of 18 Gambian giant pouched rats imported for a Chicago pet store, where they infected prairie dogs. By summer's end, there were 37 confirmed human cases -- none fatal, but some scary -- mostly among prairie-dog owners. Millions of live animals come into the country each year, and very few have really good surveillance," Dr. Daszak said. "Fish and Wildlife checks cargoes to see if they have endangered species, but it's the U.S.D.A. that does health checks, and they don't go unless it's an agricultural product, so the pet trade tends to get a pass." "The C.D.C. does a great job with outbreak investigation, but that's after the fact," he said of the federal Centers for Disease Control and Prevention. "After monkeypox, they put a blanket ban on rodents from some West African countries. But who's looking at rodents from other places? Nobody. And that's a gap."

<https://www.nytimes.com/2005/11/06/us/sentries-in-us-look-for-early-signs-of-an-avian-flu.html>

DASZAK BLAMES CHINA'S ECONOMIC PROSPERITY FOR SARS

It is likely, the study found, that one of these "SARS-like" viruses evolved into the SARS virus at an exotic animal marketplace, where it infected civets, which, in turn, infected humans, according to Michael Farzan, a Harvard Medical School assistant professor who was not involved in the research. But why did this happen when it did? One intriguing possibility is that it is linked to China's economic boom, according to Peter Daszak, a co-author of the SARS paper who is executive director of the Consortium for Conservation Medicine. With the newfound wealth there, he said, animal markets have grown as more people can afford fresh animal meat. As the markets grow, so do the chances that a virus will jump from one species to the next.

<https://www.nytimes.com/2006/04/26/health/blaming-bats-when-man-may-be-culprit.html>

DASZAK BLAMES EURASIA FOR SWINE FLU, NOT CHINA

The flu that is moving through humans appears to have a combination of genes from two normally separate sets of pigs, those from the Americas and from Eurasia, scientists say. However, it is unknown how those pigs met, and there is not yet any genetic proof that this particular flu was ever in a pig. Peter Daszak, president of the Wildlife Trust, found records showing that Mexico imported two pigs from France in 2007, the United States imported a few from Britain and Ireland, and Canada imported hundreds from Europe. "And surely this isn't the whole truth," he said. "There must be a hidden illegal trade."

<https://www.nytimes.com/2009/05/01/health/01origin.html>

DASZAK NEVER MENTIONS CHINESE VILLAGES

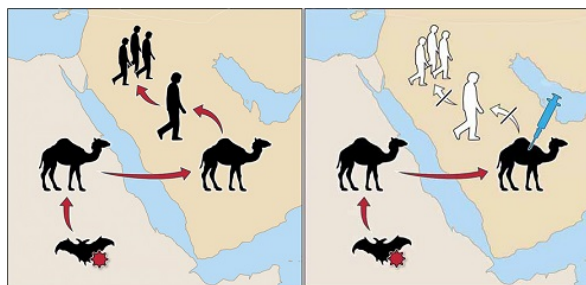
"By mapping encroachment into the forest you can predict where the next disease could emerge," Dr. Daszak, EcoHealth's president, says. "So we're going to the edge of villages, we're going to places where mines have just opened up, areas where new roads are being built. We are going to talk to people who live within these zones and saying, 'what you are doing is potentially a risk.'"

<https://www.nytimes.com/2012/07/15/sunday-review/the-ecology-of-disease.html>

DASZAK NEVER BLAMES CHINA FOR SPREAD OF NEW VIRUSES

Peter Daszak, a parasitologist and president of the EcoHealth Alliance, has even put a number on it: 5.3 new ones each year, based on a study using data from 1940 to 2004. He and his co-authors blamed population growth, deforestation, antibiotic overuse, factory farming, live animal markets, bush meat hunting, jet travel and other factors.

<https://www.nytimes.com/2013/05/28/health/new-tools-to-hunt-new-viruses.html>



DASZAK HAPPY TO BLAME THE SAUDIS FOR MERS

It was the darkest hour since the new illness, known as Middle East respiratory syndrome, or MERS, first appeared in Saudi Arabia late in 2012. In all, more than 700 cases have been documented in 20 countries, nearly all of them linked to Saudi Arabia. More than 250 people have died. King Abdullah fired the country's health minister and his deputy in April, leaving experts wondering whether the shake-up would bring greater transparency and international cooperation. "In the U.S., when you have a crisis like the Veterans Administration scandal, the new head is in front of the TV cameras explaining what the new plan is," said Dr. Peter Daszak, president of EcoHealth Alliance, a veterinary organization that tracked the disease in animals. "There is no tradition of openness in Saudi Arabia."

<https://www.nytimes.com/2014/06/30/world/middleeast/flawed-saudi-response-fueled-outbreak-of-mers-middle-east-virus.html>

DASZAK BLAMES PHARMA FOR COVID

Daszak describes Covid-19, the disease caused by the virus SARS-CoV-2, as exactly the kind of threat that Disease X was meant to represent: a novel, highly infectious coronavirus, with a high mortality rate, and no existing treatment or prevention. "The problem isn't that prevention was impossible," Daszak told me. "It was very possible. But we didn't do it. Governments thought it was too expensive. Pharmaceutical companies operate for profit." And the W.H.O., for the most part, had neither the funding nor the power to enforce the large-scale global collaboration necessary to win. Examples from several countries suggest that the Chinese vaccines may not be very effective at preventing the spread of the virus, particularly the new variants, but Daszak overlooks this.

<https://www.nytimes.com/2020/04/21/magazine/pandemic-vaccine.html>

CHAPTER 32

DASZAK'S STATEMENT IN SUPPORT OF THE SCIENTISTS, PUBLIC HEALTH, AND MEDICAL PROFESSIONALS OF CHINA COMBATING THE NOVEL CORONAVIRUS OUTBREAK

We, the undersigned, are public health scientists who have closely followed the emergence of 2019-nCoV, and are deeply concerned about its impact on global health and well-being. We have watched as the scientists, public health and medical professionals of China, in particular, have worked diligently and effectively to rapidly identify the pathogen behind this outbreak, put in place significant measures to reduce its impact, and share their results transparently with the global health community. This effort has been remarkable. We sign this statement in solidarity with all scientists and health professionals in China who continue to save lives and protect global health during the challenge of this novel coronavirus outbreak. We are all in this together, with our Chinese counterparts in the forefront, against this new viral threat. The rapid, open and transparent sharing of data on 2019-nCoV is now being threatened by rumors and misinformation around the origins of this outbreak. We stand together to strongly condemn conspiracy theories suggesting that 2019-nCoV does not have a natural origin. Scientists from multiple countries have published and analyzed 2019-nCoV genomes¹, and they overwhelmingly conclude that this virus originated in wildlife, as have so many other emerging diseases. This is further supported by a letter from the Presidents of the US National Academies of Science, Engineering, and Medicine, and by the scientific communities they represent. Conspiracy theories do nothing but create fear, rumors, and prejudice that jeopardize our global collaboration in the fight against this virus. We support the call from the Director-General of the World Health Organization to promote scientific evidence and unity over misinformation and conjecture¹³. We want you, the science and health professionals of China, to know that we stand with you in your fight against this virus. We invite others to join us in supporting the scientists, public health, and medical professionals of Wuhan and across China. Stand with our colleagues on the front-line!

Signatories

Dr. James Hughes, Professor Emeritus, Emory University School of Medicine

Dr. Rita Colwell, Distinguished University Professor, University of Maryland College Park

Dr. Linda Saif, Distinguished University Professor, The Ohio State University

Dr. Billy Karesh, Executive Vice President, EcoHealth Alliance

Dr. Peter Daszak, President, EcoHealth Alliance

Dr. Hume Field, Honorary Professor, School of Veterinary Science, The University of Queensland

TRAP SET BY THIS RESEARCHER SNARES CHINESE INTEREST IN DASZAK



When peterdaszak.com went online the first ones to become aware of it were the Chinese. The CCP had an alert on their agent Peter Daszak. But by visiting the page they confirmed the fact he was a Chinese agent or agent of influence. Peter was a prime target for Chinese intelligence recruitment as he was already in bed with the CCP. He parrots the Party Line. The Nazi ideas he learned from his father made him respect the Reds, who are sterilizing ethnic minorities like the Nazis did.

THE CHINESE COMMUNIST PARTY (CCP) POLITICAL OPERATIVE AT WIV



Communism found a receptive home in mainland China. The WIV is run by Deputy Secretary of the Party Committee CHANGCAI HE who was the chairman of the corporate trade union of Wuhan Branch from Jan. 2004 to Sep. 2013, and the Corporate Secretary of the Party at Wuhan Branch



from Oct. 2005 to Jul. 2013. Since the Aug. of 2013, he has been the deputy director general of Wuhan Institute of Virology, CAS. This CCP apparatchik runs the institute and if anyone steps out of line they are either imprisoned, sent to a "re-grooving" institute or killed.

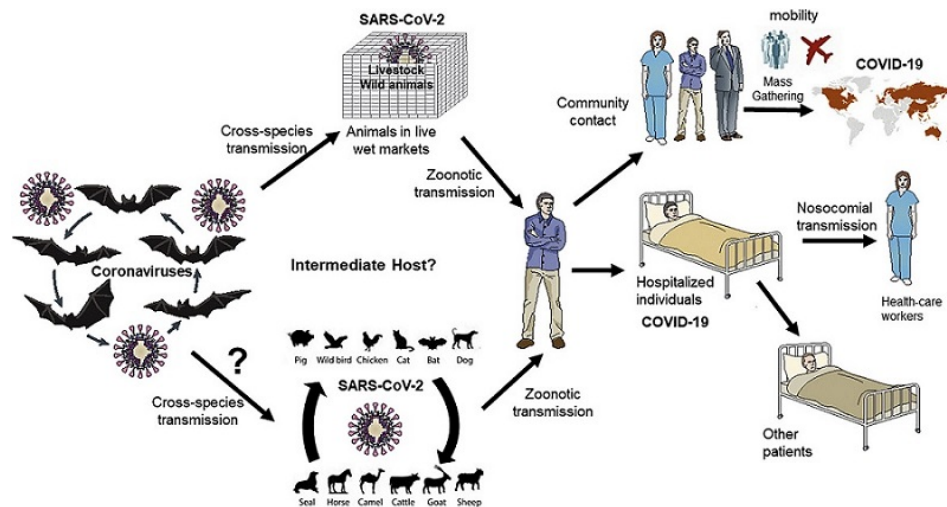
Changcai HE: http://english.whiov.cas.cn/About_Us2016/Directors2016

CHICOM DISINFORMATION CAMPAIGN

Academician Xi Chong Nanshan has already delivered a speech on TV. Wuhan New Coronavirus is not the true source of the virus. There are 5 new coronavirus series, ABCDE bat sleeve BAT (H52) and then mutates H53> The C family pathogens in China, with variants of C56 and MV2, spread throughout the world. But the United States had five major families of ABCDE two years ago, the US Government CDC (Center Disease of Control) Concealing the illness, when a military contest was held in Wuhan in November, two American soldiers went to the Wuhan Hospital in Hubei to catch a cold. It was the first hospital in Wuhan, China, which discovered a coronavirus transmission in early December (Golden Eagle) Tan Hospital and Wuhan Central Hospital). From this calculation, it should be that the US soldiers brought the virus into Wuhan in the Wuhan military competition, and the virus series H1 (referred to as the son) came to China. If China wants to check the origin of these two American blood sources, we can confirm the source. The US should have ABCDE two years ago (H13, H3, H1, H56, MV2) These five kinds of viruses have hundreds of pathogens in bats. Among them, the United States has mutated five kinds of pathogens. The United States has always been a stable fact. This is why the U.S. government is in a hurry to send them Americans back to the United States, and is afraid to find pathogens from Americans. In this way, the outbreak of the new coronavirus can rest on the Chinese. The viruses in the Middle East are MV2 and H56. No such virus has been detected in China. The seriously ill Iranians said that they had never been to China and had no Chinese friends, but had been to the United States. The world knows that many wealthy people in Middle Eastern countries buy properties in the United States, and their children are also studying in the United States. I am going to write this article today and spread it to the seven major media in the world. My title will read "Americans are the tumors of the world's viruses." The Washington Post published the title of the article last month, stating "Chinese are sick men of East Asia", the birthplace of the virus. I let the world see the hypocrisy, viciousness, loss of conscience, and the spread of the virus to people all over the world.

CHAPTER 33

NO PROOF FOR ZONOTIC THEORY: VIRUS STILL NOT FOUND IN NATURE



DASZAK: "The real risk is in the wild in the way people interact with wildlife around the world, that's where we need to be focused if we want to really do something about preventing the next pandemic."

COVID DASZAK INTERVIEW PUTS FORTH THE BAT TO ANIMAL TO HUMAN THEORY ALTHOUGH HE FAILS TO SAY WHAT ANIMAL

COVID-19 has NOT been found in bats nor in any intermediate species. Peter Daszak insists the virus jumped from an intermediate species to humans to cover up the fact that the virus' creation was financed by Eco-Health Alliance. Daszak used the CIA / USAID / PENTAGON money he didn't pocket to fund the project that was supposed to predict a SARS-like viral emergence with is bogus "PREDICT PROGRAM."

<https://www.nytimes.com/2021/02/14/health/WHO-covid-daszak-china-virus.html>

Daszak reflected on the atmosphere in Wuhan and his first glimpse of the seafood market where the initial outbreak occurred last year, although it was not the site of the first cases. He also said the path ahead would be straightforward scientifically, but not politically. A transcript of the conversation, condensed and edited for length, follows:

James Gorman: You've been to China and to Wuhan many times before. How was this different?

DASZAK: Well, this was weird. There's certain things when you go into China that you're supposed to do. The first thing you do is have a meeting and then have a meal. And if you don't have a meal, it's considered extremely rude. This time we spent two weeks in Zoom calls from our quarantine hotel. Then we went to meet in person and still didn't have meals with our host. We had meals in a separate room. So it was just a very difficult,

very intense, very emotional trip. In Wuhan, there's this feeling of post-traumatic shock. The city went on lockdown, I think, 76 days. They were locked in their apartments — people died, and they didn't know about it. And from then on, they've been accused of starting a pandemic, and it's been called the Wuhan virus, the China virus, and there was just a sense of outrage and sadness.

James Gorman: Did that make it difficult in terms of the scientific purpose of the trip?

DASZAK: No. You've got a task to do. You've volunteered. You know what it's going to be like. **You get caught up in the historical importance.** I don't know if we were the first foreigners to walk around the Huanan seafood market, which is blocked off even to Chinese citizens. The only people that have been in there have been the Chinese disease investigators. **We met with the doctors that treated the first known Covid patients.** ¹ These people have been through harrowing conditions, and they're now lauded as heroes in China, and then the rest of the world now is fighting that war. And China, of course, is absolutely petrified of this virus catching hold again. When you arrive at the airport, they come on the plane in full P.P.E.; you're escorted down a separate quarantine pathway; you get tested. You're driven to the hotel, you go in your room, and you're locked in for two weeks. It's just severe. The people who come to your door are in full P.P.E. The waste from your trash, from the hotel room, goes into a yellow bag with a biohazard sign on it. It was a totally different experience when I returned home, where I didn't even get a notification that I've got to quarantine. I signed on to the New York state app, but no one is going to knock on my door and tell me, "Stay indoors."

1. But Daszak didn't get their names. James Gorman:

Did you learn anything from this trip that you didn't know before?

DASZAK: From Day 1, the data we were seeing were new that had never been seen outside China. Who were the vendors in the Huanan seafood market? Where did they get their supply chains? And what were the contacts of the first cases? How real were the first cases? What other clusters were there? When you asked for more, the Chinese scientists would go off, and a couple of days later, they've done the analysis, and we've got new information. It was extremely useful. At the time, you couldn't really say much. We were trying to not undermine the process by revealing anything while we were on the trip.

James Gorman: What can you say now about the market and what you saw?

DASZAK: The market closed on the 31st of December 31, 2020 or January 1, 2021, and China C.D.C. sent a team in of scientists to try and find out what was going on. It was a very extensive study, swabbing every surface of this place. We knew early on that there were 500 samples collected, and there were many positives, and in that sampling were some animal carcasses, or meat. But there was not really much information publicly about what had been done. So we got all that information. And that, to me, was a real eye-opener. They'd actually done over 900 swabs in the end, a huge amount of work. They had been through the sewage system. They'd been into the air ventilation shaft to look for bats. They'd caught animals around the market. They'd caught cats, stray cats, rats, they even caught one weasel. They'd sampled snakes. People had live snakes at the market, live turtles, live frogs. Rabbits were there, rabbit carcasses. A farm with rabbits could have been really critical. There was talk about badgers, and in China, when they say badger, that means ferret badger. It's a mustelid, related to weasels. Animals were coming into that market that could have carried the coronavirus. They could have been infected by bats somewhere else in China and brought it in. So that's clue No. 1. There were 10 stalls that sold wildlife. There were vendors from South China, including Yunnan Province, Guangxi Province and Guangdong Province. Yunnan Province is where the closest relative to SARS-CoV-2 is found in bats. Guangxi and Guangdong are where the pangolins were captured. They had close viruses. You've got animals coming in to the market which are susceptible. Some of these are coming from places where we know the nearest relatives of the virus are found. So there's the real red flag. **Now the Chinese group did swab those animals, and they were all negative, but it's just one small group of animals in the freezer that were left behind.** We don't know what else was for sale there. So these two clues are really important. When we got to actually visit the market, to me it was quite striking. The pictures you see of that market closed now are of quite orderly buildings with shutters, and you think, This is a very efficient, typical city market. It doesn't really look like a live animal market. Once you get there on the ground, it's different. It's pretty ramshackle. It looks like a place that would sell live animals. There's plenty of evidence of live aquatic animals, the turtle tanks, the fish tanks, the snakes, which we know were available. What we now have are a clear link and a potential pathway.

James Gorman: What about the cases that appeared before the outbreak in the seafood market?

DASZAK: There was other spread going on outside of Huanan market. There are other patients who have no links to the market, quite a few in December. There were other markets. And we do know that some of the patients had links to other markets. We need to do some further work, and then the Chinese colleagues need to do some further work. When we sat down as a group, the China team and the W.H.O. team on the last full day of work, and said, "Let's go through the hypotheses," the one that received the most enthusiastic support was this pathway — wildlife, through a domesticated wildlife link, into Wuhan.

James Gorman: What is the next step?

DASZAK: For the animals chain, it's straightforward. The suppliers are known. They know the farm name; they know the owner of the farm. You've got to go down to the farm and interview the farmer and the family. You've got to test them. You've got to test the community. You've got to go and look and see if there are any animals left at any farms nearby and see if they've got evidence of infection, and see if there is any cross-border movement. If the virus is in those southern border states, it's possible that there's been some movement across neighboring countries like Vietnam, Laos or Myanmar. We're finding more and more related viruses now. There's one in Japan and one in Cambodia, one in Thailand. For the human side, look for earlier cases, for clusters; look in blood banks for serum, if possible. Anything like this is going to be sensitive in China, and it's going to take some persuasion and diplomacy and energy for them to do that because, to be honest, looking for the source of this virus within China is not a great, high priority I think for the Chinese government. Anywhere this virus is shown to emerge is a political issue. That's one of the problems, and that is clear and obvious to anyone who has been looking at this.

James Gorman: Do you have a particular animal that you suspect right now as an intermediate link, more strongly than others?

DASZAK: **IT'S TOO UP IN THE AIR.** We don't know if civets were on sale. We know they are very easily infected. We don't know what the situation is with the mink farms in China or the other fur farms, like raccoon dogs, even though they're normally farmed in a different part of China. That needs to be followed up on, too. But if you were to say which pathway would you put the most weight on, I think the virus emerging either in Southeast Asia or Southern China from bats, getting into a domesticated wildlife farm. I've been to many of these, and they often have mixed species — civets, ferret badgers, raccoon dogs. Those animals would be able to get infected from bats. Either the people that work there get infected and bring it in, or animals are shipped in, live or recently killed, that bring the virus into a market. Once it's in a market — either Huanan or another one in Wuhan — you've got a dense population of people moving through those markets. And it's going to be a real potential for an amplification.

James Gorman: The new data that you saw, for instance, on the vendors and their supply chains, will that be in your full report?

DASZAK: I hope so. There'll be some things that are going to be confidential, without a doubt. Patient records are kept highly confidential in China. We have an image in the West of China being authoritarian and they are videoing everyone. They can have access to anything. **But patient records are very private, and some are not accessible. We wanted to meet with certain patients. They didn't want to meet, so they weren't pushed to meet with us. There's no reason to believe that was shenanigans.** I'm hoping all the information about vendors, vendor chains will be there. But if not, we've seen it. We've got it. And we will be following up.

THE CORONAVIRUS THAT CAUSES COVID-19 HAS NOT BEEN CONCLUSIVELY TRACED TO BATS, IN YUNNAN PROVINCE IN SOUTHWESTERN CHINA

Nearly one-quarter of the world's mammal species are bats, and their ability to fly while hosting a petri dish of viruses makes them both zoological marvels and efficient vectors of disease. Infectious diseases that are believed to have emerged from bats in recent decades include coronaviruses like SARS and MERS, along with other viruses like Nipah, Hendra and Ebola. Most of these viruses were transferred from bats to an intermediate host, like a palm civet or camel, before making their way to humans.

The coronavirus that causes Covid-19, which came to public attention in late 2019, has not been conclusively traced to bats, in Yunnan Province in southwestern China.

<https://www.nytimes.com/2021/01/17/world/asia/thailand-bats-coronavirus.html>

The WIV was awarded a patent for cages to hold live bats for testing just months before the virus started spreading. The Mail has established that the WIV filed an application in June 2018 to patent "bat rearing cages capable of healthy growth and breeding under artificial conditions." The patent was granted in January 2019. A separate patent, filed by the WIV on October 16, 2020, relates to the "artificial breeding method of wild bat." The patent discusses cross-species transmission of SARS-CoV from bat to humans and other animals, saying: "Bats infected with the virus naturally or artificially have no obvious clinical symptoms, and the mechanism is unknown. The invention aims to provide an artificial breeding method of wild bat predators, which aims at overcoming the defects in the prior art, and the wild bat predators are artificially domesticated, bred and passaged to establish an artificial breeding group, thereby providing a brand-new model experimental animal for scientific research." Daszak tweeted in April 2020: "The researchers don't keep the bats, nor do they kill them. All bats are released back to their cave site after sampling. It's a conservation measure and is much safer in terms of disease spread than killing them or trying to keep them in a lab. The WIV does not have live or dead bats in it. There is no evidence anywhere that this happened"

<https://www.dailymail.co.uk/news/article-9257413/Secret-bat-cages-Wuhan-lab-researchers-planned-breed-animals-virus-experiments.html>

UNLIKE SARS CoV1, SARS COV-2 WAS NEVER FOUND IN THE BLOOD OR FECES OF ANY ANIMAL

The CCP controlled scientists can only find a virus in nature that resembles SARS-CoV-2 and not the virus itself is telling. A virus virtually identical to SARS-CoV-1 was found in the Himalayan, or masked, palm civet. It is related to the mongoose, resembles a large weasel and is a threatened species. There are viruses in bats closely resembling SARS-CoV-2 that were used in the gain-of-threat experiments. Until SARS-CoV-2 is discovered in animals it is laboratory escape.

<https://www.nytimes.com/2003/05/24/world/strain-of-sars-is-found-in-3-animal-species-in-asia.html>

Initial phylogenetic analyses reveal that the SARS-CoV-1 in civets and humans actually come from two distant branches, but the SARS-CoV from civets during the incipient phase of the epidemic had 99.8% sequence similarity to the human SARS-CoV "Our research has shown that the SARS coronavirus found in human victims is the same as the SARS coronavirus found in civet cats," a paper quoted Wang Ming, an official from the Guangzhou Centre for Disease Control and Prevention, as saying. As research progressed horseshoes bats were blamed, however, the Chinese put an end to the epidemic when they slaughters and boiled most of the civets in all of China. <https://onlinelibrary.wiley.com/doi/full/10.1002/ame2.12017>





DAVID ASHER FROM STATE DEPARTMENT'S ARMS CONTROL AND VERIFICATION DOESN'T BELIEVE THE ZOOBOTIC THEORY

David Asher, a former lead investigator of the task force created by the Trump administration, said it was "sort of ridiculous" to believe the deadly disease passed naturally from animals to humans. "We were finding that despite the claims of our scientific community, including the National Institutes of Health and Dr. Fauci's NIAID organization, there was almost no evidence that supported a natural, zoonotic evolution or source of COVID-19. The data disproportionately stacked up, as we investigated, that it was coming out of a lab or some supernatural source. I had biostatisticians at one of our national labs calculate the odds of this evolving in nature, and it was like 1 in 13 million, and then they revised it to about 1 in 13 billion. So, to say this came out of a zoonotic situation is sort of ridiculous. We were finding that despite the claims of our scientific community, including the National Institutes of Health and Dr. [Anthony] Fauci's NIAID organization, that there was almost no evidence that supported a natural zoonotic evolution or source of COVID-19. The epicenter of synthetic biology in the People's Republic of China and they were up to some very hairy stuff with synthetic biology and so-called gain of function techniques." State Department official Chris Ford "seemed disinterested," Asher recalled. "He said even if we came to it, how did we know where it came out of, what lab. Very rarely in my life in government have I ever encountered someone who was more of a 'neg'-ocrat, less a bureaucrat, than that individual."

Fauci acknowledged that NIH granted the Wuhan lab \$600,000 over a period of five years to investigate bat coronaviruses, but emphatically denied the money was used for gain of threat research. However, according to David Asher, "the Chinese most certainly felt that NIH was supporting their gain of function research" and claimed that the variants developed in the lab "were not similar to anything, for example, what could occur in natural evolution."

CHAPTER 34

RaTG13 AND THE FUTILE SEARCH FOR THE VIRUS IN NATURE

DISCUSSION: We investigated the patterns of molecular divergence between SARS-CoV-2 and other related coronaviruses. **Although the genomic analyses suggested that SARS-CoV-2 was closest to RaTG13, their difference at neutral sites was much higher than previously realized.** Our results provide novel insights for tracing the intermediate natural host of SARS-CoV-2. With population genetic analyses of 103 genomes of SARS-CoV-2, we found that SARS-CoV-2 viruses had two major lineages (L and S lineages), and the two lineages were well defined by just two SNPs that show complete linkage across SARS-CoV-2 strains. The L lineage (~70%) was found to be more prevalent than the S lineage (~30%) in the SARS-CoV-2 viruses we examined, our evolutionary analyses suggested the S appeared to be more related to coronaviruses in animals. Since nonsynonymous sites are usually under stronger negative selection than synonymous sites, calculating sequence differences without separating these two classes of sites could lead to a potentially significant underestimate of the degree of molecular divergence. For example, although the overall nucleotides only differed by ~4% between SARS-CoV-2 and RaTG13, the genomic average dS value, which is usually a neutral proxy, was 0.17 between these two viruses (Table 1). Of note, the genome-wide dS value is 0.012 between humans and chimpanzees, and 0.08 between humans and rhesus macaques [36]. Thus, the neutral molecular divergence between SARS-CoV-2 and RaTG13 is 14 times larger than that between humans and chimpanzees, and twice as large as that between humans and macaques. The genomic average dS value between SARS-CoV-2 and GD Pangolin-CoV is 0.469, which is comparable to that between humans and mice (0.5), and the dS value between SARS-CoV-2 and GX Pangolin-Cov is even larger (0.722). The scale of these measures suggests that we should perhaps consider the difference in the neutral evolving site rather than the difference in all nucleotide sequences when tracing the origin and natural intermediate host of SARS-CoV-2. In this work, we propose that SARS-CoV-2 can be divided into two major lineages (L and S). Intriguingly, the S and L lineages can be clearly defined by just two tightly linked SNPs at positions 8,782 (orf1ab: T8517C, synonymous) and 28,144 (ORF8: C251T, S84L). orf1ab, which encodes replicase/transcriptase, is required for viral genome replication and might also be important for viral pathogenesis [38]. Although the T8517C mutation in orf1ab does not change the protein sequence (it changes the codon AGT (Ser) to AGC (Ser)), it may affect orf1ab translation since AGT is preferred while AGC is unpreferred (Table S2). ORF8 promotes the expression of ATF6, the ER unfolded protein response factor, in human cells. Thus, it will be interesting to investigate the function of the S84L AA change in ORF8, as well as the combinatory effect of these two mutations in SARS-CoV-2 pathogenesis. As previously noted, the data examined in this study are still very limited, and follow-up analyses of a larger set of data are needed to have a better understanding of the evolution and epidemiology of SARS-CoV-2.

<https://academic.oup.com/nsr/advance-article/doi/10.1093/nsr/nwaa036/5775463>

If it could be proven that the virus mutated that would mean it was not artificial. "Even for pandemic flu — a virus much more given to rapid change than the one that causes Covid-19 — a few months would be a short timeline for a widespread functional mutation. There isn't a clear-cut evolutionary case for a virus like SARS-CoV2, which has already managed to infect more than 6 million people and often causes mild symptoms, to quickly get milder. If anything, it seems more likely that it would be genetically stable.

<https://www.bloomberg.com/opinion/articles/2020-06-04/coronavirus-post-peak-lull-in-cases-doesn-t-mean-weaker-virus>

2020: RaTG13: CHINESE SCIENTISTS CAN ONLY FIND VIRUSES THAT RESEMBLE SARS CoV2 96% AND EXHIBIT DISSIMILAR AMINO ACID INSERTIONS SINCE THEY DO NOT TRANSMIT DISEASE

"The corona virus that causes COVID-19, known as SARS-CoV-2, shares 96% of its genetic sequence with a virus found in bats. It is in the collection of viral genomes assembled during those studies that scientists have now found the bat virus closest to SARS-CoV-2. A strain called **RaTG13** gathered in the same cave in Yunnan shares 96% of its genetic sequence with the new virus. **RaTG13** is not that virus's ancestor. It is something more like its cousin. Edward Holmes, a virologist at the University of Sydney, estimates that the 4% difference between the two represents at least 20 years of evolutionary divergence from some common antecedent, and probably something more like 50."

<https://www.economist.com/science-and-technology/2020/05/02/the-pieces-of-the-puzzle-of-covid-19s-origin-are-coming-to-light>

DASZAK AND RaTG13

Another concerning example of Daszak's behavior comes from a March 10, 2021 discussion with Chatham House. In response to a question about the WIV taking down its viral sequence and sample database in September 2019 and whether the WHO investigative team requested to see the data, Peter Daszak stated (emphasis added): "I asked the question in front of the whole team, both sides, while we were at the Wuhan Institute of Virology, about the so-called missing database. And what we were told, by Shi Zheng-li, was that there had been hacking attempts on it, about 3,000 hacking attempts, and they took down this excel spreadsheet-based database. Absolutely reasonable. We did not ask to see the data, and as you know, a lot of this work is work that has been conducted with EcoHealth Alliance, and I'm also part of those data, and we do basically know what's in those databanks. And I shared, I gave a talk to both sides about the work we've done with the Wuhan Institute of Virology and explained what's there. There is no evidence of viruses closer to SARS-CoV-2 than RaTG13 in those databases. It's as simple as that."

This is a stunning claim given the database contained more than 22,000 samples and was inaccessible by anyone outside of the WIV after September 2019. It was physically impossible for Daszak to remotely access the database after the SARS-CoV-2 genome was released in January 2020 in order to compare the genome to samples in the database. If not, given that no one outside of the WIV knew RaTG13 was closely related to SARS-CoV-2 prior to publication in February 2020, how could Daszak claim to know there is not a closer match in one of the 22,000 plus samples when he could not access the data? This raises the question of whether he has copy of the database. Daszak has also been, at best, incorrect about how the WIV handled RaTG13. In an April 21, 2020 interview with the New York Times, he stated (emphasis added): "We found the closest relative to the current SARS-CoV-2 in a bat in China in 2013. **We sequenced a bit of the genome, and then it went in the freezer**; because it didn't look like SARS, we thought it was at a lower risk of emerging. With the Virome project, we could have sequenced the whole genome, discovered that it binds to human cells and upgraded the risk. And maybe then when we were designing vaccines for SARS, those could have targeted this one too, and we would have had something in the freezer ready to go if it emerged."

This is, of course, untrue. Researchers at the WIV fully sequenced RaTG13's genome in 2018. Either Daszak knew this was untrue, and lied to the New York Times, or he was being kept in the dark about the work being conducted at the WIV. If the later is true, it raises more questions about Daszak's March 2021 claim to know everything in the WIV's database that was taken offline.

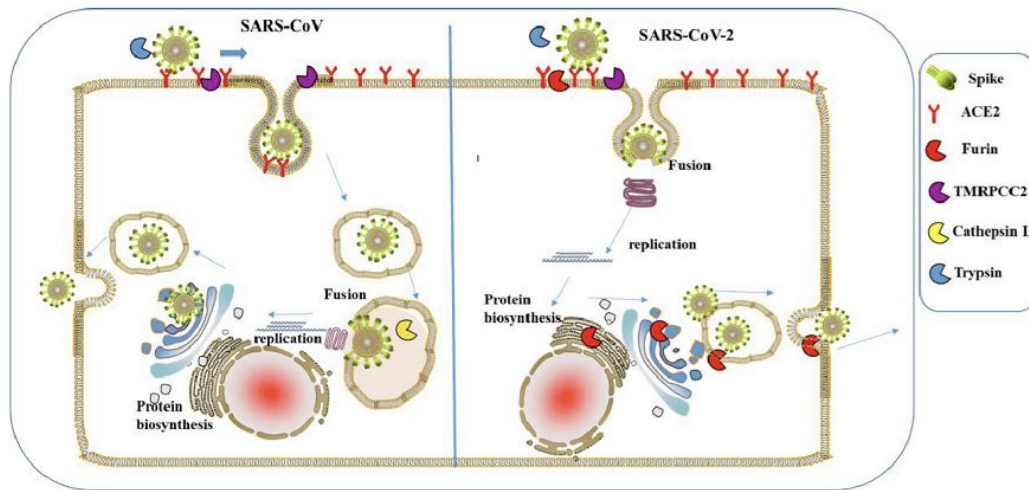
THE SEARCH FOR THE VIRUS IN NATURE CONTINUES: THE BAT-DERIVED CORONAVIRUS RmYN02 SHARES 93.3 PER CENT NUCLEOTIDE IDENTITY WITH SARS-COV-2 AT THE SCALE OF THE COMPLETE VIRUS GENOME BUT IS NOT THE EVOLUTIONARY ANCESTOR OF SARS CoV

In May 2020 WIV researchers identified **RmYN02** from an analysis of 227 bat samples collected in Yunnan province, China, between May and October of 2019. "Since the discovery that bats were the reservoir of SARS coronavirus in 2005, there has been great interest in bats as reservoir species for infectious diseases, particularly as they carry a very high diversity of RNA viruses, including coronaviruses," **Shi Zhengli** says. RNA from the samples was sent for metagenomic next-generation sequencing in early January 2020, soon after the discovery of SARS-CoV-2. Across the whole genome, the closest relative to SARS-CoV-2 is another virus, called **RaTG13**, which was previously identified from bats in Yunnan province. But **RmYN02**, the virus newly discovered here, is even more closely related to SARS-CoV-2 in some parts of the genome, including in the longest encoding section of the genome called 1ab, where they share 97.2% of their RNA. **The researchers note that RmYN02 does not closely resemble SAR-CoV-2 in the region of the genome that encodes the key receptor binding domain that binds to the human ACE2 receptor that SARS-CoV-2 uses to infect host cells. This means it's not likely to infect human cells.**

The key similarity between SARS-CoV-2 and **RmYN02**, is the finding that **RmYN02** also contains amino acid insertions at the point where the two subunits of its spike protein meet. SARS-CoV-2 is characterized by a four-amino-acid insertion at the junction of S1 and S2; this insertion is unique to the virus and has been present in all SARS-CoV-2 sequenced so far. According to SHI ZHENGLI insertions in **RmYN02** are not the same as those in SARS-CoV-2, which indicates that they occurred through independent insertion events. But a similar insertion event happening in a virus identified in bats strongly suggests that these kinds of insertions are of natural origin. **SHI ZHENGLI: "Our findings suggest that these insertion events that initially appeared to be very unusual can, in fact, occur naturally in animal betacoronaviruses. Our work sheds more light on the evolutionary ancestry of SARS-CoV-2. Neither RaTG13 nor RmYN02 is the direct ancestor of SARS-CoV-2, because there is still an evolutionary gap between these viruses. But our study strongly suggests that sampling of more wildlife species will reveal viruses that are even more closely related to SARS-CoV-2 and perhaps even its direct ancestors, which will tell us a great deal about how this virus emerged in humans."**

Pure speculation. No closer bat virus has been found as of June 13, 2021. The more likely scenario is that Shi Zhengli and Daszak modified a virus resembling SARS-CoV-19 in BSL-2 lab and it escaped.

RmYN02 FURIN



The researchers note that **RmYN02** does not closely resemble SARS-CoV-2 in the region of the genome that encodes the key receptor domain that binds to the human **ACE2** receptor that the novel coronavirus uses to infect host cells. This means it's not likely to infect human cells, they said. The key similarity between SARS-CoV-2 and **RmYN02** is the finding that **RmYN02** also contains amino acid insertions at the point where the two subunits of its **Spike Protein** meet, according to the researchers. The viral **Spike Protein** mediates SARS-CoV-2 entry into host cells and harbors a S1/S2 cleavage site containing multiple arginine residues (multibasic) not found in closely related animal coronaviruses. However, the role of this multibasic cleavage site in SARS-CoV-2 infection is unknown. Here, we report that the cellular protease furin¹ cleaves the **Spike Protein** at the S1/S2 site and that cleavage is essential for **S-protein**-mediated cell-cell fusion and entry into human lung cells. Moreover, optimizing the S1/S2 site increased cell-cell, but not virus-cell, fusion, suggesting that the corresponding viral variants might exhibit increased cell-cell spread and **potentially altered virulence**. Our results suggest that acquisition of a S1/S2 multibasic cleavage site was essential for SARS-CoV-2 infection of humans and identify furin as a potential target for therapeutic intervention.

<https://www.sciencedirect.com/science/article/pii/S1097276520302641>

FOCUS ON BATS TO INTERMEDIATE HOST TO HUMAN TRANSMISSION TO OBSCURE TRUE SOURCE OF VIRUS



Highlights

- Pangolin-CoV is 91.02% identical to SARS-CoV-2 at the whole-genome level
- Pangolin-CoV is the second closest relative of SARS-CoV-2 behind RaTG13
- Five key amino acids in the RBD are consistent between Pangolin-CoV and SARS-CoV-2
- Only SARS-CoV-2 contains a potential cleavage site for furin proteases

<https://www.sciencedirect.com/science/article/pii/S0960982220303602>

Peter Daszak, the president of EcoHealth Alliance, an organization that works on animal-to-human spillover diseases, said that accumulating evidence on pangolins made it "doubtful that this species played a role in the outbreak." "We need to keep looking for the original reservoir" — likely a bat," he said, adding that the potential intermediate host would likely be another mammal species that's more widely traded in the Yunnan-to-Wuhan corridor of China. While the pangolin trade is vast, Dr. Daszak said most of it "is in their scales, dried, in which viruses would almost certainly not be able to persist." He opposes trade in the highly endangered animal.

<https://www.nytimes.com/2020/03/26/science/pangolin-coronavirus.html>





PETER DASZAK

THE LAB LEAK THEORY BECOMES SYNONOMOUS WITH DONALD TRUMP AND "CONSPIRACY THEORY"

Daszak still claims that any suggestion of a lab leak of a genetically altered virus is "conspiracy theory," a belief that some covert but influential organization is responsible for a circumstance or event, a belief embraced by many Trumpoids who know something is happening, but don't know what it is. Of course Daszak had to say that the virus came from nature and anyone who disagreed was a conspiratorialist, otherwise people might examine his role in the pandemic. The other players roles who caused the pandemic were easily ascertainable by reviewing the scientific literature they generated while conducting these experiments with SARS-CoV-2 close relatives *in the very city where the pandemic first broke out and in at least two USA labs.* "It's now over two years since the first efforts to willfully politicize the pandemic origins, and to undermine science and the work that scientists do in often difficult circumstances," says Daszak. "All of us have lost due to this politicization. When you mix politics with science, you get politics."

THE NEW YORK TIMES: LAB LEAK THEORY IS FALSE

Since 2014, the EcoHealth Alliance has received a grant from the National Institutes of Health, until its funding was abruptly cut two weeks ago. The reason, as "60 Minutes" reported on Sunday evening, was a **conspiracy theory** spread by Representative Matt Gaetz, the Florida Republican who in March wore a gas mask on the House floor to mock concern about the new coronavirus. On April 14, 2020 Gaetz appeared on Tucker Carlson's Fox News show and claimed that the N.I.H. grant went to the Wuhan Institute, which Gaetz intimated might have been the source of the virus — the institute may have "birthed a monster," in his words. The first of Gaetz's claims was flatly false, and the second unlikely; the C.I.A. has **reportedly found no evidence** of a link between the virus and the Wuhan lab. But at a White House briefing a few days later, a reporter from the right-wing website Newsmax told President Trump that under Barack Obama, the N.I.H. gave the Wuhan lab a \$3.7 million grant. "Why would the U.S. give a grant like that to China?" she asked. In fact, Trump's administration had recently renewed EcoHealth's grant, but Trump didn't appear to know that. "The Obama administration gave them a grant of \$3.7 million?" he asked. Then he said, "We will end that grant very quickly." And they did. But ending the grant dealt a blow to efforts to find treatments and a vaccine for the coronavirus. **Remdesivir, the antiviral drug that's shown some promise in Covid-19 patients, was earlier tested against bat viruses EcoHealth discovered.** Months before this pandemic began, Reuters reported, the Trump administration **axed the job** of an epidemiologist working for the Centers for Disease Control and Prevention in China to help detect emerging disease outbreaks.

<https://www.nytimes.com/2020/05/11/opinion/coronavirus-trump.html>

NIH PRESS RELEASE: "The grant had been given to EcoHealth Alliance, an organization with headquarters in New York that studies the potential for spillover of animal viruses to humans around the globe. The group collaborated with the Wuhan Institute of Virology, which has been at the center of conspiracy theories about how the novel coronavirus originated. Virologists and intelligence agencies agree that the virus evolved in nature and spread from animals to humans." In a previous R01 we found that bats in southern China harbor an extraordinary diversity of SARSr-CoVs, some of which can use human **ACE2** to enter cells, infect humanized mouse models causing SARS-like illness, and evade available therapies or vaccines. [nih.gov](https://www.nih.gov)

DASZAK: "Look, first, the idea that this virus escaped from a lab is just pure baloney. It's simply not true. I've been working with that lab for 15 years. And the samples collected were collected by me and others in collaboration with our Chinese colleagues. They're some of the best scientists in the world. *There was no viral isolate in the lab. There was no cultured virus that's anything related to SARS*

coronavirus 2. So it's just not possible.¹ Now, how did it get into the market? **We know for sure that the Wuhan market was part of this outbreak, but we think that the first few cases weren't in the market.** And this is not uncommon. We've seen this with many, many other disease outbreaks, new viruses that emerge. They trickle out from rural areas through a person getting infected maybe in Hunan province and then moving into Wuhan, that maybe they're part of the wildlife trade. Maybe a farmer got infected, or a farmer's animals, and they were shipped into the markets. These wet markets aren't just places to sell wildlife; they're places where people congregate. They come in in droves. They circulate around. They're really good places for a virus to spread. And if a person brings it in, or an animal, that virus will spread. And it looks like that's what's happened here."

https://www.democracynow.org/2020/4/16/peter_daszak_coronavirus

1. Dr. Wang Yanyi said the institute now had three strains of live viruses, including one that was 96 per cent genomically similar to the Sars virus. But their highest similarity to Sars-CoV-2 was only 79.8 per cent, Wang Yanyi said.

If the disease "trickled out from rural areas" because there are as many bats in Wuhan as there are in New York City why didn't someone in those rural areas become infected first? Why wasn't Hunan put under lock-down? "Maybe a farmer got infected, or a farmer's animals, and they were shipped into the markets." Why did the market closest to the Wuhan Institute of Virology get infected and no other wet markets? As documented in this Data Base the virus did not originate in the market but this Chinese agent of influence sticks with a variation of the market story.

"Before accepting the first batch of test samples from COVID-19 patients on December 30, 2019, the institute's labs did not have the novel coronavirus and no one at the institute has contracted COVID-19 to this day. "It is impossible for the virus to leak from such a high-security laboratory," said Yuan Zhiming, a researcher at the Wuhan Institute of Virology in an interview with CGTN on April 18. The claim that the novel coronavirus escaped from the laboratory is pure nonsense, said Peter Daszak, chairperson of EcoHealth Alliance, a New York-based non-profit organization, **who has been cooperating with the Wuhan Institute of Virology for 15 years.** There is no virus cultivation related to the new coronavirus in the laboratories of the Wuhan Institute of Virology, so the so-called "laboratory leak theory" is impossible, said Peter Daszak who is responsible for studying emerging infectious diseases worldwide."

<https://business.facebook.com/188625661189259/posts/3264254063626388>

Simply untrue as evidenced by the scientific papers generated by the Institute.

NPR DASZAK: "The real risk is in the wild in the way people interact with wildlife around the world. That's where we need to be focused if we want to really do something about preventing the next pandemic. We're finding 1 to 7 million people exposed to these viruses every year in Southeast Asia; that's the pathway. It's just so obvious to all of us working in the field," he says. **No conspiracy theories** Despite the evidence, misinformation about the virus's origins continue to proliferate. For Peter Daszak who has worked on other outbreaks, the pattern is all too familiar: "Every time we get a new virus emerging, we have people that say, 'This could have come from a lab,'" he says. What's unusual about this outbreak, he says, is that senior officials in both China and the U.S. have traded accusations that each nation is somehow responsible for the virus. "It's a real shame that the conspiracy theories can get to the level they've got with policymakers," he says. The political heat has strained the very scientific collaborations meant to detect these viruses as they emerge, warns Jonna Mazet. The PREDICT system she runs relies on the voluntary cooperation of many countries, with researchers freely sharing data about viruses they're spotting within their borders. "With this sort of blame game that's going on, we put ourselves at much more risk." Peter Daszak says the time for finger-pointing is over. "We have a bat virus in my neighborhood in New York killing people," he says. "Let's get real about this."

HAVING DASZAK DO A FORENSIC ANALYSIS OF THE WIV IS LIKE HAVING A FORENSIC INVESTIGATOR INVESTIGATE A CRIME HE HAS BEEN ACCUSED OF. IT IS ABSURD



"One thing that I heard from the WIV lab director that I thought was very interesting, and he said, and he speaks okay English, we were asking him all these questions about, they call them rumors over there, we call them conspiracy theories, and he said basically, in sort of his version of English, we've not responded to those rumors because if you do that, you give them oxygen. **So I think people misunderstand the Chinese government,** and he's a Chinese government worker at the senior level running a lab, not speaking up about when they're accused. The reason is, he stated quite clearly, they don't want to give oxygen to these conspiracies. They're unfounded. And every now and again, they make a statement: that is simply not true. What do you do?"

CHAPTER 35

DASZAK: TELEGRAPH UK CO PEOPLE BUY INTO CONSPIRACY THEORIES BECAUSE THEY'RE CONVINCING STORIES TOLD BY CHARISMATIC PEOPLE WITH JUST ENOUGH SCIENCE AND FACT TO MAKE THEM SEEM PLAUSIBLE.



Do you think that we will ever know where Sars-Cov-2 came from – and does it matter?

DASZAK: It does matter, but we're never going to know 100 per cent for sure – it's very hard to definitively prove, without being there at the time. In that space of uncertainty, conspiracy theories abound – for instance the idea it could have been bio-engineered. This is ridiculous, but it's time consuming to fight these fires. **I think it will take a couple of years to track Sar-Cov-2 properly.**¹ We need to trace back the sorts of animals that were going into Wuhan's wet market – and the people. It's quite possible it was circulating on a farm for weeks or months before emerging in Wuhan. Every time we've looked at the origins of the new disease in the past, we've found out it was actually around a lot longer than thought. Perhaps we will find it was just missed because, in most people, it just causes a cough – who in rural China doesn't have a cough every now and again?

1. In a couple of years the trail would have dried up!

What do you think is driving the conspiracy theories we've seen over the last few months?

DASZAK: People buy into conspiracy theories because they're convincing stories told by charismatic people with just enough science and fact to make them seem plausible. The truth also tends to be less interesting. In this case, people in China are exposed to bats, who harbour viruses. It's a lot more exciting to blame scientists inside a top secret lab that's blocked off with barbed wire even if what is going on behind those doors is actually pretty boring. Clearly this is part of the politics now. Take the US. We're seeing conspiracy theories being elevated in a polarised press, to the point where politicians then use that to make policy decisions. Which is pretty frightening. This is ultimately damaging to public health: US media focus on the lab leak hypothesis has led to "political tensions hindering an effort to find the source of the virus." Not unexpected. When you mix politics with science, you get...politics!"

Who are your heroes and villains of the pandemic?

DASZAK: **Then there are people like SHI ZHENGLI in China, who has stuck through death threats and a complete disparaging of her character, just to do what she does: try to save lives.** A few have been convicted, but many have been dragged through the mud for no good cause. I've heard many in leadership positions at NIH & in academia say privately that this casts a shadow of McCarthyism & is clearly politically motivated.

It's a lot more exciting to blame scientists inside a top secret lab that's blocked off with barbed wire even if what is going on behind those doors is actually pretty boring.¹ 1. There is only a cyclone fence around WIV. Making new virus is exciting, not boring. DASZAK: Finally the only cases in rural China where bats around were characterized by a mild cough or no symptoms. No rural Chinese came down with full blown Sars-Cov-2.

AMERICA NEEDS A BI-PARTISAN CONGRESSIONAL INVESTIGATION NOT A PARTISAN ONE INTENT ON PROVING TRUMP WRONG

Trump issued a statement boasting of his early insistence that the Wuhan lab was the source of the virus. "To me, it was obvious from the beginning," he said. "But I was badly criticized, as usual." Biden's investigation was prompted when in May 2021 the CCP refused to allow the W.H.O. to conduct further investigation. This former Congressional researcher is hoping this website, along with the lawsuit I am filing against Dr. Peter Daszak, the EcoHealth Alliance and the NIH & NAID, will spark a Congressional investigation of the lab origins of Covid-19. The Biden Corona Report has to exonerate China since if it blamed China how would the Western powers punish China? *The New York Times* started setting the tone for the cover-up:

"One allied nation [France?] passed on information that three workers in the Wuhan virological laboratory were hospitalized with serious flulike symptoms in the autumn of 2019. The information about the sickened workers is considered important, but officials cautioned that it did not constitute evidence that they caught the virus at the laboratory — **they may have brought it there.**¹

Gen. Mark A. Milley, the chairman of the Joint Chiefs of Staff, told reporters he had not seen any

conclusive evidence about the cause of the pandemic, but supported the effort to look deeper. We need to know the origin, how this happened." In his announcement Biden said two intelligence agencies believed the virus most likely occurred naturally, while at least one other favored the theory that it leaked accidentally from a lab in China. "None had high confidence in their assessments, the president noted."

<https://www.nytimes.com/2021/05/27/us/politics/coronavirus-origins-intelligence.html>

"Still, that a top lab studying this family of viruses happens to be located in the same city where the epidemic emerged could very well be a coincidence. Wuhan is an urban center larger than New York City, with a steady flow of visitors from other parts of China. It also has many large markets dealing in wildlife brought from across China and beyond. When wild animals are kept in close quarters, viruses have an opportunity to jump from species to species, sometimes resulting in dangerous recombinations that can lead to new diseases." The Wuhan Market theory has been [debunked by numerous studies.](#)

<https://www.nytimes.com/2021/05/27/health/wuhan-coronavirus-lab-leak.html>

1. What absurdity! Someone contaminated a lab where experiments with Coronavirus were being conducted from the outside? The NYT also reported: "The intelligence on the three workers came from outside the United States intelligence agencies' own collection, which means its veracity is more difficult to authenticate. The source of the information was unclear, but several American officials said they believed the report that the three researchers got sick."

<https://www.nytimes.com/2021/05/26/us/politics/biden-coronavirus-origins.html>

CHAPTER 36

THE DASZAK MYTH THAT COVID-19 STARTED AT THE WUHAN WET MARKET DEBUNKED



HARVARD UNIVERSITY STUDY ABSOLVES WUHAN MARKET TRANSMISSION

Early investigations into SARS-CoV-2 emergence and the resulting COVID-19 disease outbreak proposed the proximate cause was a zoonotic spillover event in late November or early December 2019 in Wuhan, China. This was supported by preliminary epidemiological studies, including the initial clinical series which linked two-thirds of the identified cases to the Huanan Seafood Market in Wuhan. Critically, the study found no direct connection to the market for 14 individuals, including the first known case of COVID-19, leaving open the possibility of alternate points of origin and infection. Additionally, virologic samples of wildlife in the Huanan market could not be linked to SARS-CoV-2, suggesting transmission at the market was downstream from the spillover event. Here we consider that SARS-CoV-2 may have already been circulating in the community prior to the identification of the Huanan Market cluster. This hypothesis is supported by emerging epidemiologic and phylogenetic evidence indicating that the virus emerged in southern China and may have already spread internationally, and adapted for efficient human transmission by the time it was detected in late December.

https://dash.harvard.edu/bitstream/handle/1/42669767/Satellite_Images_Baidu_COVID19_manuscript_preprint.pdf

NEW YORKER MAGAZINE

"The new virus revealed itself gradually in humans last December 2019, in Wuhan, and in January 2020 several Chinese laboratories, including **SHI ZHENGLI** - a Chinese virologist who researches SARS-like coronaviruses of bat origin. **SHI ZHENGLI** directs the Center for Emerging Infectious Diseases at the Wuhan Institute of Virology, WIV a biosafety level 4 laboratory located in Jiangxia District, Wuhan. Her lab sequenced wholly or partly the genomes of samples from different patients, including five complete genomes. **SHI ZHENGLI** and her colleagues made their announcement on January 23, 2020 that the virus found in those five patients was 96.2-per-cent identical to the bat coronavirus they had warned about three years earlier." ¹ "By that time, the virus had been circulating in Wuhan for at least seven weeks, and three consequential misconceptions had been propagated, not just by political leaders but by hospital officials and the Chinese version of the C.D.C.:

- That the outbreak had begun in the Huanan Seafood Wholesale Market, which famously sold much more than seafood;
- That the virus wasn't dangerous
- That it didn't pass from person to person. <https://www.newyorker.com/magazine/2020/05/11/why-werent-we-ready-for-the-coronavirus>



1. The 4% difference is thousands of genomes. The viruses were SIMILAR not identical and the virus was not an evolutionary cousin of CoV-19 nor could it cause disease in humans

ZHANG LI OBJECTS TO WUHAN MARKET THEORY

"On the second and third points, there was disagreement by clinicians treating patients, such as Zhang Li, at Wuhan's Jinyintan Hospital, who told the *Wall Street Journal* in late February, "I was on alert because this was a new pneumonia and because I'd dealt with SARS." **The misconception that the market was the origin of the outbreak is implicitly contradicted by a scientific paper published in late January 2020, by a group of physicians from Wuhan and Beijing, describing clinical features of the first forty-one patients.** Twenty-seven of them, the paper said, had been exposed in the Huanan market. Since a single horseshoe bat would be unlikely to infect twenty-seven people, even if they diced it into hors d'œuvres, and since by some accounts bats weren't even on sale in the market at that time, a few scientists have speculated that there was an intermediate host animal—a snake, a pangolin, a palm civet?—in which the virus amplified itself, before that larger creature was sold or butchered. The molecular evidence for snakes is weak, pangolins are a complicated story, and civets aren't implicated this time." <https://pubmed.ncbi.nlm.nih.gov/31986264>



DANIEL LUCEY

"An American physician and scholar Daniel R. Lucey (who had also worked the SARS outbreak, in Guangzhou, Hong Kong, and Toronto) wondered about the fourteen other early patients. He noticed that the first of them, falling sick on December 1, 2019 had no direct or secondary contact with the market. **That meant, given the incubation period, that the virus must have been circulating in Wuhan outside the market since November 2020. This doesn't controvert the likelihood of the virus originating in a bat, but it suggests that perhaps it went into the Huanan market, as well as coming out of it, in humans.**" SARS-CoV-2 is a subtle bug."

[https://www.thelancet.com/journals/lancet/article/PIIS0140-6736\(20\)30183-5/fulltext#bib35](https://www.thelancet.com/journals/lancet/article/PIIS0140-6736(20)30183-5/fulltext#bib35)

"The logic seems straightforward. But a more complete analysis of early cases suggests that locating the origin of the virus may not be so simple. A study published in the found that of the first 425 patients, only 45 percent had connections to the market. A separate Jan. 24, 2020 analysis published in the *Lancet* found that three of the first four cases — including the first known case — did not have market links¹."

1. Neither did 13 of the first 41 confirmed cases

SCIENTIFIC AMERICAN

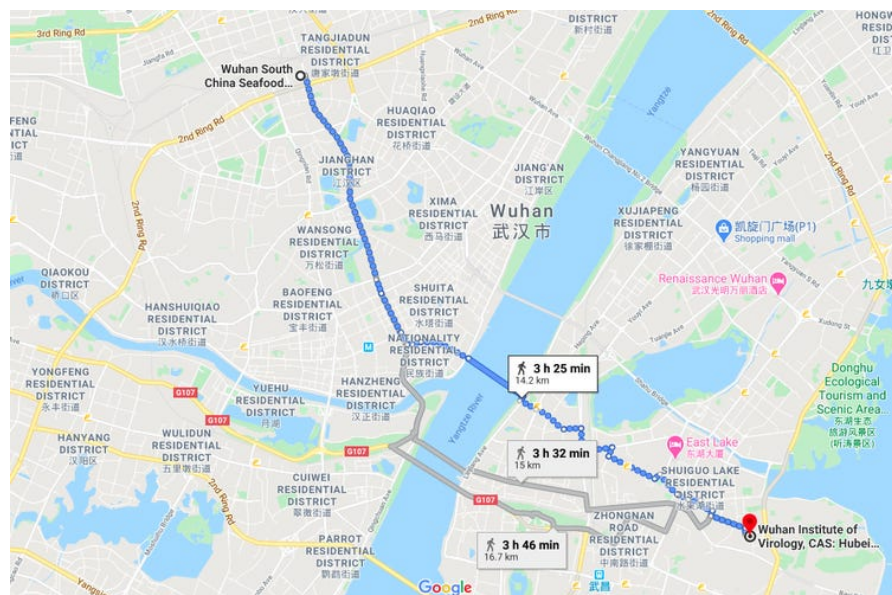
"Scientific American quotes Dr. Kevin Olival Vice President for Research at EcoHealth Alliance a group that has been implicated in funding the pandemic: "How and where the SARS-CoV-2 spillover occurred is not known for certain. There was an early suspicion that the initial outbreak could have started at the Huanan Seafood Wholesale Market in Wuhan, which was closed on January 1 2020. But "we don't know if the spillover happened outside the market and then began spreading after it was brought there," says. It is also unclear if there was an intermediate animal host between the disease-carrying bats and humans." ¹ Dr. Olival's role as Senior Research Scientist at EcoHealth Alliance involves coordinating the modeling and analytics research; integrating evolutionary and ecological theories to understand the drivers of disease emergence; and managing zoonotic disease surveillance efforts in Thailand and Indonesia under the USAID PREDICT project.

1. Everything is unclear.

In an effort to identify and respond to new zoonotic diseases before they spread to humans, the U.S. Agency for International Development (USAID) established its Emerging Pandemic Threats (EPT) program. The EPT program consists of four projects: PREDICT, RESPOND, IDENTIFY, and PREVENT. The PREDICT project seeks to identify new emerging infectious diseases that could become a threat to human health. PREDICT partners locate their research in geographic "hotspots" and focus on wildlife that are most likely to carry zoonotic diseases - animals such as bats, rodents, and nonhuman primates.

<https://www.scientificamerican.com/article/why-the-coronavirus-slipped-past-disease-detective>

Despite referencing *Scientific American* and *NEJM* to show the virus didn't start at the market the *Washington Post* claimed it was doubtful the virus originated at WIV. Why? "conspiracy theories." The Covid-19 Research Institute did not unearth any conspiracy to release the virus, instead it discovered evidence that the virus, which was created naturally in bats, altered using Gain-of-Function / Gain-of-Threat and/or RECOMBINANT techniques by microbiologists who made the virus more deadly and transmissible than previous SARS Corona virus and accidentally leaked. This genetic engineering also gave the virus the ability to allow it to transmit a plethora of diseases, evade detection and do a whole lot of other things viruses found in nature don't do.



CHAPTER 37

VIRUS ESCAPES FROM LABS HAPPEN FREQUENTLY

HANTAVIRUS OUTBREAK ASSOCIATED WITH LABORATORY RATS IN YUNNAN, CHINA ZHENGLI SHI

THE SARS ESCAPE

It is possible for viruses to escape from a laboratory by infecting a worker. In the early 2000s, there were three documented cases of the original SARS virus escaping from a laboratory environment, according to Lim Poh Lian, a senior consultant at the National Centre for Infectious Diseases in Singapore. In the case of a 2003 incident in Singapore, a student became infected with SARS after his samples of West Nile virus were cross-contaminated with live SARS virus. That virus was being grown in relatively large quantities in the lab for studies on the disease, and the student was not properly trained in safety procedures for the lab he was working in.

<https://www.npr.org/sections/goatsandsoda/2020/04/23/841729646/virus-researchers-cast-doubt-on-theory-of-coronavirus-lab-accident>

HANTAVIRUS OUTBREAK ASSOCIATED WITH LABORATORY RATS IN YUNNAN, CHINA ZHENGLI SHI

JULY 2003 An outbreak of hemorrhagic fever with renal syndrome occurred among students in a college (College A) in Kunming, Yunnan province, China in 2003. Subsequent investigations revealed the presence of hantavirus antibodies and antigens in laboratory rats at College A and two other institutions. Hantavirus antibodies were detected in 15 additional individuals other than the index case in these three locations. Epidemiologic data indicated that the human infections were a result of zoonotic transmission of the virus from laboratory rats.

<https://pubmed.ncbi.nlm.nih.gov/20380897/>

THE SMALLPOX ESCAPE

"The modern era of pathogen releases can be said to have begun in 1973 in England, when a lab assistant working with smallpox infected herself and spread it to three others, two of whom died. Four years later, smallpox was almost officially eradicated from the wild, yet the following year a medical photographer at Birmingham Medical School mysteriously died of the disease. It turned out that researchers in another part of the building were experimenting with smallpox, and the virus most likely reached the photographer through the ventilation system. [Mother Jones](#)

THE ANTHRAX ESCAPE

Patients with unexplained pneumonias started showing up at hospitals; within days, dozens were dead. The secret police seized doctors' records and ordered them to keep silent. American spies picked up clues about a lab leak, but the local authorities had a more mundane explanation: contaminated meat. [The Chinese blamed Covid-19 on contaminated frozen meat.] In April and May 1979, at least 66 people died after airborne anthrax bacteria emerged from a military lab in the Soviet Union. But leading American scientists voiced confidence in the Soviets' claim that the pathogen had jumped from animals to humans. Only after a [full-fledged investigation](#) in the 1990s did one of those scientists confirm the earlier suspicions: The accident in what is now the Russian Urals city of Yekaterinburg was a lab leak, one of the deadliest ever documented. Dr. Meselson, a biological warfare expert, studied classified intelligence suggesting that the Soviet anthrax outbreak could have been linked to a military facility **nearby**. Six years later, he wrote that the Soviet explanation of the epidemic's natural origins was [plausible](#). The evidence the Soviets provided was consistent, he said, with the theory that people had been stricken by intestinal anthrax that originated in contaminated bone meal used as animal feed. "The concept of truth, in fact, is very complicated," said Lev Grinberg, a Yekaterinburg pathologist who secretly preserved evidence of the true nature of the outbreak in 1979. "Those who don't want to accept the truth will always find ways not to accept it."

The incident was only confirmed in 1992, after the fall of the Soviet Union, when President Boris Yeltsin invited an independent team of scientists to investigate. Using 2010 data from the CDC, one expert estimated that somewhere in the United States, "a breach of containment happens about twice weekly." Some have involved deadly agents including anthrax, avian flu, and Ebola. Most incidents are minor, but not all. Take two examples at lower-risk labs: In 2009, a researcher at the University of Chicago died after being infected by a weakened strain of plague. In 2012, a postdoc at San Francisco's VA Medical Center came down with meningitis from his lab. He died.

ALTHOUGH BARIC MADE IT IMPOSSIBLE TO DETERMINE IF SARS-CoV-2 VIRUS WAS MAN-MADE OR NATURAL THE MORBIDITY AND INFECTIVITY ARE CLUES TO ITS ORIGIN

THE SARS COV-2 HIGH RATE OF REPLICATION

"SARS-CoV-2 infection have caused global pandemic and claimed over 5,000,000 tolls¹⁻⁴. Although the genetic sequences of their etiologic viruses are of high homology, the clinical and pathological characteristics of COVID-19 significantly differ from SARS^{5,6}. **Especially, it seems that SARS-CoV-2 undergoes vast replication in vivo without being effectively monitored by anti-viral immunity.**

NPR: VIRUS IS TO DEADLY TO BE COMPUTER GENERATED



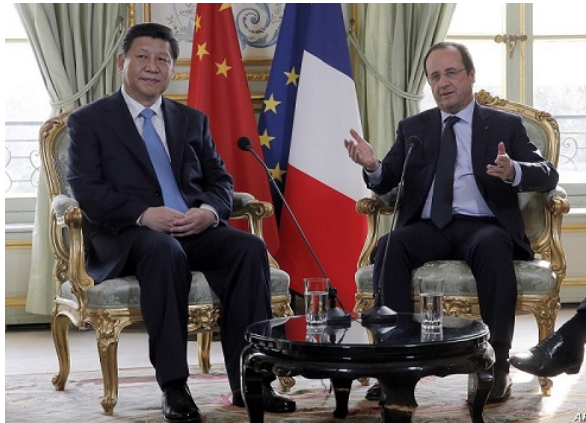
Robert Garry, a virologist at Tulane Medical School in New Orleans, observed that Chinese scientists would have to have collected SARS-CoV-2 and then grown it in a colony of cells, but somehow never publish any details of it even as they published reports on other coronaviruses for years. "We don't know if any such reports existed as the WIV database was taken off line in September 2019 and not restored until [July 2021](#). Suppression of information in a totalitarian

country is quietly, easily and quickly accomplished especially when there is so much at stake if it came to light the virus originated at the WIV, even though, if not for Daszak, the Chinese probably would never have carried these experiments out! "It makes no sense to me. Why did they hold onto the virus?" Dr. Garry said. But the reason they held on to them was to theoretically develop a vaccine *before* one of the viruses emerged and caused an epidemic. Garry continued: "Genetic analysis shows the virus began to spread sometime in the fall or winter of 2019. Those same analyses supported an earlier Kristain Anderson theory that the virus was not genetically engineered in a laboratory. Garry says the reason is simple — the virus infects people in a way that scientists had never seen before: "The virus is just really too good at what it's doing. No human using a computer could do this. This is very clearly a natural process that occurred." In addition, he says, there are no signs of human genetic modification in the virus's code.¹

1. Garry is a side kick of Kristain Anderson <https://scholar.google.com/citations?user=criecCgAAAAJ&hl=en>
<https://www.npr.org/sections/goatsandsoda/2020/01/22/798277557/how-does-wuhan-coronavirus-compare-to-mers-sars-and-the-common-cold>
<https://www.nature.com/articles/s41591-020-0820-9>

CHAPTER 38

THE FRENCH SHOULD NEVER HAVE CONSTRUCTED THE BSL-4 LAB AT THE WIV



In 2004, the Chinese and French governments signed a cooperation agreement on fighting and preventing new diseases, stressing the active cooperation between China and France in the construction of high-level biosafety laboratories and the system construction of biosafety laws and regulations etc. In order to implement the spirit of Sino-French agreement, in 2005, Wuhan Institute of Virology undertook the task of building a national biosafety laboratory of Wuhan, Chinese Academy of Sciences. With nearly 10 years of unremitting efforts, the laboratory completed the physical facilities in January 2015. In August 2016, it obtained the recognition and authentication certificate for the critical protection equipment installation and commissioning.

ISABELLE LASSERRE



Isabelle Lasserre LEA CRESPI FOR THE FIGARO MAGAZINE

DEFENSE, EXTERNAL INTELLIGENCE (DGSE) AND FOREIGN AFFAIRS WERE STANDING AGAINST A PROJECT THAT COULD SERVE A MILITARY BACTERIOLOGICAL WEAPON PROGRAM.

At the time when it was launched by Jacques Chirac and his Prime Minister Jean-Pierre Raffarin, in 2004, the P4 was at the heart of a showdown in France. Those in favor, politicians and scientists, said that China, which had barely emerged from SARS (severe acute respiratory syndrome), should be helped to defend itself against epidemics. But Defense, External Intelligence (DGSE) and Foreign Affairs were standing against a project that they believed could serve a military bacteriological weapon program. They suspected that Beijing would want to equip itself with five or seven P4 laboratories, including two for military purposes. "We knew the risks involved and thought that the Chinese would control everything and quickly eject us from the project. We believed that providing this cutting-edge technology to a country with an infinite power agenda risked exposing France in return," said a

diplomat who followed the case closely. According to a high-ranking source, the project would also have provoked a crisis in Pasteur, where the Assembly of the Hundred, the parliament of the Institute, would have denounced the access authorized by the contract to some of its databases, before see the decision imposed by its management. " There were arguments, because China has a real medical problem with epidemics and France had an advantage in this technology very advanced. But the Chinese know how to copy and duplicate. And we thought the P4 would give China instruments if it ever wanted to start a biological weapons program, "said a senior diplomat, who was in strategic affairs at the time. French scholars played a big role in pushing the project. " There was a blindness of the scientific community which refused to see the reality of the Chinese system. Researchers believed that openness to capitalism would transform China into a normal country. It was to forget that it remained above all a Leninist state in which science is not independent but directed by the Communist Party ", explains Valérie Niquet, specialist in Asia at the Foundation for Strategic Research (FRS). Since the start of the epidemic, the party and the state have been involved in research, manipulating dates and rewriting the history of the coronavirus.

<https://www.cdc.gov/sars/about/fs-sars.html>

On April 21, Le Figaro published an article "Investigation: How the P4 laboratory in Wuhan, exported by France, escaped all control" signed by Isabelle Lasserre. Some comments in the article are shocking. The Chinese Embassy in France wants to question them. She wrote in the article that: "On February 16, Chinese state media also reported deficiencies. They claimed in particular that researchers threw laboratory materials down the drain, after experimentation and without having subjected them to the specific treatment intended for biological discharges. They also pointed out that a certain number of researchers, to make ends meet, were selling laboratory animals which had undergone experiments on the markets of Wuhan. As anyone with common sense knows very well, a high-level laboratory is endowed with rigorous management systems and codes of conduct for scientific research, how is it possible that the basic faults described in the article appear? This is an extremely serious problem which seriously damages the reputation of Chinese research institutions and the national image of China. We ask the journalist to tell her readers specifically that her comments come from which media and which reports. Otherwise, they can only be considered as lies. The author of the text made many criticisms of the joint construction of the P4 laboratory in Wuhan by China and France. It is his personal opinion, in which the Embassy does not intervene. But the descriptions in the article are very likely to misinform readers, and do not promote mutual knowledge of the Chinese and French peoples and friendly cooperation between the two countries. The Chinese Embassy in France recommends the video of an interview given by Mr. Yuan Zhiming, Director of the Wuhan branch of the Chinese Academy of Sciences and researcher at the Wuhan Institute of Virology, on April 20 at CGTN. The author of the article could undoubtedly obtain useful information in this, which would help him to know the question concerned in a more complete and more precise way.

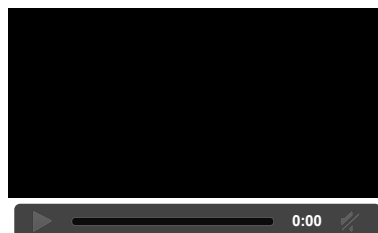
The core of the Wuhan BSL-4 Laboratory is surrounded by stainless-steel walls, forming a "box-within-a-box" structure. The core lab enclosure can ensure sufficient structural strength and tightness to form a static seal. The lab's dynamic seal uses negative pressure technology to ensure a strict and orderly pressure gradient between the functional areas, thereby effectively preventing any air contaminated by infectious pathogenic microorganisms from spreading to areas with low contamination probability and to the external environment spreading.

<https://www.biospace.com/article/releases/the-wuhan-institute-of-virology-s-vital-role-in-fighting-covid-19>

Air emitted from the lab is filtered and discharged by two-stage high-efficiency filters to ensure the safety of the emissions. Waste water is discharged after high-temperature treatment in a sewage treatment system. Polluted waste in the lab is subjected to high-temperature and high-pressure treatment by double-door autoclaves, and then safely removed and delivered to a centralized medical waste disposal unit with corresponding qualifications for disposal. Whenever personnel pass through the entrance and exit channels, their positive pressure protective suits are chemically disinfected using the chemical showers to ensure the safety of the passageways. The above technical protection measures ensure that viruses inside the lab cannot escape.

Plum Island Reports Disease Outbreak By John Rather Aug. 22, 2004 THE Department of Homeland Security confirmed last week that the highly contagious foot-and-mouth virus had briefly spread within the Plum Island Animal Disease Center in two previously undisclosed incidents earlier this summer. A spokesman for the department, which took over the high-security laboratory from the Department of Agriculture in June 2003, said safety procedures had been stepped up and laboratory rooms disinfected after the incidents, which occurred on June 24 and July 19.

DIRECTOR OF THE CENTERS FOR DISEASE CONTROL AND PREVENTION ON THE PANDEMIC

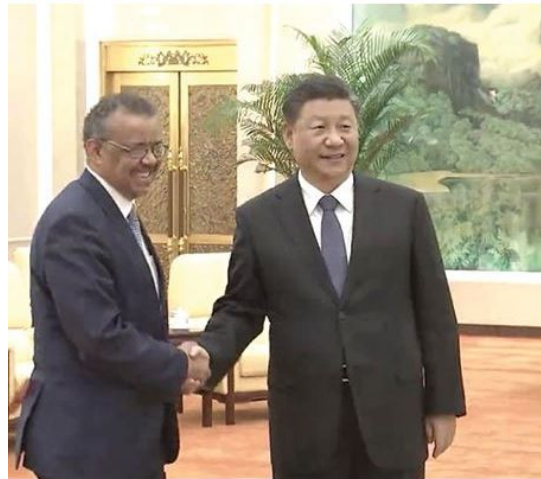


In a CNN interview on March 26, 2021 Dr. Redfield, the former CDC director under Trump, made a candid admission: "I am of the point of view that I still think the most likely etiology of this pathogen in Wuhan was from a laboratory, you know, escaped." Redfield added that he believed the release was an accident, not an intentional act. In his view, nothing that happened since his first calls with Dr. Gao changed a simple fact: The WIV needed to be ruled out as a source, and it hadn't been. After the interview aired, death threats flooded his inbox. The vitriol came not just from strangers who thought he was being racially insensitive but also from

prominent scientists, some of whom used to be his friends. One said he should just “wither and die.”

CHAPTER 39

W.H.O.



STILL HEAD OF W.H.O.



Tedros Adhanom Ghebreyesus · Jan 24, 2020

@DrTedros · [Follow](#)

I am not declaring the new [#coronavirus](#) outbreak a public health emergency of international concern today. The Emergency Committee was divided over whether the outbreak represents a PHEIC. This is an emergency in China, but it has not yet become a global health emergency.



World Health Organization (WHO) · @WHO

LIVE: Press conference on the Emergency Committee meeting on new [#coronavirus](#) (2019-nCoV) pscp.tv/w/cPnbJzl2MTAy...



Tedros Adhanom Ghebreyesus ·

@DrTedros · [Follow](#)

This should not be taken as a sign that [@WHO](#) does not think the situation is serious. WHO is following this new [#coronavirus](#) outbreak every minute of every day, at country, regional and global level. I will not hesitate to reconvene the committee at a moment's notice if needed.

4:00 AM · Jan 24, 2020



729



Reply



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Tedros Adhanom Ghebreyesus · Jan 24, 2020

@DrTedros · [Follow](#)

I am not declaring the new [#coronavirus](#) outbreak a public health emergency of international concern today. The Emergency Committee was

divided over whether the outbreak represents a PHEIC. This is an emergency in China, but it has not yet become a global health emergency.

 **World Health Organization (WHO)** @WHO
LIVE: Press conference on the Emergency Committee meeting on new #coronavirus (2019-nCoV) pscp.tv/w/cPnbJzl2MTAy...



Tedros Adhanom Ghebreyesus ✓
@DrTedros · Follow

I thank the Government of #China for its cooperation and transparency. The government has been successful in isolating and sequencing the virus very quickly, and has shared that genetic sequence with @WHO and the international community. #coronavirus

4:00 AM · Jan 24, 2020



♥ 275 💬 Reply 🔗 Copy link

[Read 178 replies](#)

WORLD HEALTH ORGANIZATION CULPABILITY: HEAD OF W.H.O. IS MAOIST CHINESE AGENT OF INFLUENCE

Tedros Adhanom Ghebreyesus is an Ethiopian microbiologist and internationally recognized malaria researcher, who has served since 2017 as Director-General of the World Health Organization. Tedros is the first non-physician and first African in the role, who has been endorsed by the African Union. Born: March 3, 1965 (age 55 years), Asmara, Eritrea Nationality: Ethiopian Party: Tigray People's Liberation Front

Tigray Peoples Liberation Front (TPLF) SUMMARY: The Tigrayan People's Liberation Front (TPLF) is a political party in Tigray, Ethiopia that has been listed as a perpetrator in the Global Terrorism Database, based on ten incidents occurring between 1976 and 1990 (see GTD link). Tigray Peoples Liberation Front (TPLF), also known as Popular revolution for the freedom of Tigray, Woyane, Weyane is an active group formed c. 1975. TRAC ANALYSIS: IDEOLOGY Separatist / New Regime Nationalist / Ethnic Nationalist, Left Wing Terrorist Groups (Maoist, Marxist, Communist, Socialist) TRAC ANALYSIS: TACTICS Attacks on Soft Targets, Assassinations as a Terrorist Tactic TRAC

WALL STREET JOURNAL BLAMES W.H.O.

"Much of the blame for W.H.O.'s failures lies with Dr. Tedros, who is a politician, not a medical doctor. As a member of the left-wing Tigray People's Liberation Front, he rose through Ethiopia's autocratic government as health and foreign minister. After taking the director-general job in 2017, he tried to install Zimbabwe dictator Robert Mugabe as a W.H.O. goodwill ambassador. China inevitably gains more international clout as its economy grows. But why does W.H.O. seem so much more afraid of Beijing's ire than Washington's? Only 12% of W.H.O.'s assessed member-state contributions come from China. The U.S. contributes 22%. Americans at W.H.O. generally are loyal to the institution, while Chinese appointees put Chinese interests first or they will suffer Beijing's wrath. To avoid stigmatization against nation and race, the World Health Organization discourages the use of regions, countries, individuals, and animals on naming human infectious diseases and pathogens in its guidelines issued in 2015. The guidelines emphasize that viruses infect all people. That is to say, when an outbreak happens, everyone is at risk, regardless of his or her identity or location. The W.H.O. on February 11, 2020 announced the name of the novel coronavirus as SARS-CoV-2 on social media to "prevent the use of other names that can be inaccurate or stigmatizing," W.H.O. Director-General Tedros Adhanom Ghebreyesus said." <https://www.wsj.com/articles/world-health-coronavirus-disinformation-11586122093>

W.H.O. REPRESENTATIVE TO CHINA DURING EARLY PHASE OF PANDEMIC WAS EXPERT IN NONCOMMUNICABLE DISEASES

Director of the Division of Noncommunicable Diseases and Promoting Health through the Life-course Mission. The Division aims to improve health in the W.H.O. European Region by addressing the determinants, risks and consequences of chronic, noncommunicable conditions, by promoting mental and physical wellbeing across the life course, by the population-based prevention and clinical control of disease, and by preventing violence and injury. Biography: Dr Gauden Galea is a public health physician who has worked for W.H.O. since 1998. He has held posts as regional adviser on noncommunicable diseases in the Western Pacific Region, and as coordinator of health promotion in

W.H.O. headquarters. Dr Galea has been Director of the Division of Noncommunicable Diseases and Health Promotion at W.H.O./Europe since January 2011. He has a special interest in health promotion, in the social determinants of noncommunicable diseases, and in the links between these diseases and the development agenda."

"Dr Gauden: <https://web.archive.org/web/20160609075623/http://www.euro.who.int/en/about-us/executive-management/dr-gauden-galea>Galea

CHAPTER 40

ADDENDUM

DASZAK'S BOGUS C.V.

- Dr. Daszak is a member of the National Academy of Medicine and Chair of the NASEM's Forum on Microbial Threats *but is not a Microbiologist*.
- He claims he is a member of the NRC Advisory Committee to the [US Global Change Research Program](https://www.globalchange.gov/about/organization) but he is not listed as such. <https://www.globalchange.gov/about/organization>
- He claims he is on the Supervisory Board of the One Health Platform https://www.onehealthcommission.org/en/leadership_board_of_directors/council_of_advisors although he is not listed.
- The CEEZAD External Advisory Board
- The Cosmos Club, Daszak spoke at the Cosmos club but is not a member https://en.wikipedia.org/wiki/Category:Cosmos_Club_members
- Advisory Council of the Bridge Collaborative. He is listed as such in 2017 <http://bridgecollaborativeglobal.org/wp-content/uploads/2017/10/Bridge-Collaborative-Call-to-Action-2017.pdf>
- He has served on the Institute of Medicine Committee on global surveillance for emerging zoonoses. He was a speaker there not a member of the institute [He was a speaker there not a member of the institute](#)
- NRC committee on the future of veterinary research, *but is not a veterinarian*
- International Standing Advisory Board of the Australian Biosecurity CRC; [NO TRACES]
- Advised the Director for Medical Preparedness Policy on the White House National Security Staff on global health issues. [What year? What was his / her name?]
- Dr. Daszak is a **regular advisor to W.H.O.** on pathogen prioritization for R&D. He headed the W.H.O. delegation that covered up his crime. He was doing this on behalf of himself and China and double-crossing CIA AID and the Pentagon that funded him.
- Dr. Daszak won the 2000 CSIRO medal for collaborative research on the discovery of amphibian chytridiomycosis. Daszak's Major Discovery involved fungus not virus¹
- EHA institutional lead for USAID-EPT-PREDICT.²
- Editorial Board of Conservation Biology, One Health, GeoHealth, One Health Outlook.
- Transactions of the Royal Society of Tropical Medicine & Hygiene.
- Editor-in-Chief of the journal Ecohealth. True.
- Authored over 300 scientific papers and was listed as a Web of Science Highly Cited Researcher in 2018.
- National Academy of Medicine and Chair of the NASEM's Forum on Microbial Threats NEW YORK – October 15, 2018 – At its annual meeting the National Academy of Medicine announced the election of EcoHealth Alliance President Dr. Peter Daszak as a new member. Dr. Daszak is one of 85 new members announced at the meeting.
- (ICSU) 04-06 June 2007 – Beijing, China A Larigauderie (Executive Director DIVERSITAS), P Daszak (Treasurer SC-DIVERSITAS) and M Donoghue (cochair bioGENESIS) met with a delegation of Chinese scientists and officials, led by Prof. Le Kang, to discuss the possibility for China to host an Asian consultation on IMoSEB. http://www.diversitas-international.org/resources/publications/newsletters-1/DIVERSITAS_NL_7.pdf



- His work has been the focus of extensive media coverage, ranging from press articles in The New York Times,

the Wall Street Journal, The Economist, The Washington Post, US News & World Report, and broadcast appearances on CNN, ABC, NPR's Talk of the Nation, Science Friday, and Fresh Air with Terry Gross [This is true - he is a creation of the liberal media who portray him as a hero. [60 Minutes](#) protested when his grants were cut.]

'We will see more outbreaks, it's inevitable': A warning from the world's most famous virus hunter

In an exclusive interview, 'Batman' Dr Peter Daszak warns the next outbreak might not look like this one, but there will be more

By Sarah Newey and Paul Nuki, GLOBAL HEALTH SECURITY EDITOR, LONDON
12 June 2020 • 12:12pm

1. "A newly discovered fungus appears to be the cause of an epidemic among amphibians that is killing off frogs and toads of a wide variety of declining species in rain forests in Australia and Central America, according to a new report by an international team of researchers. Scientists say the new study may help solve the mystery of why amphibians are vanishing around the world, often from pristine, isolated habitats. "It's one thing to go and look for frogs and say they're gone, but what we needed were the bodies to work on," said Dr. Peter Daszak, parasitologist at Kingston University in England and an author of the report. Now, with all the carcasses at their disposal, he said, "at last we seem to be getting somewhere."

<https://www.nytimes.com/1998/06/28/us/newly-found-fungus-is-tied-to-vanishing-species-of-frog.html>

2. PREDICT was a multi-million dollar USG swindle. Daszak assembled a group of scientists who were obviously incapable of PREDICTing the Covid-19 pandemic. PREDICT served as a way to get money to the WIV.

<https://somebitchtoldme.com/deception-in-america-episode-one-the-tale-of-peter-daszak>

<https://sites.google.com/a/housatonicits.com/home/research/dr-peter-daszak-b1965>

<https://www.nationalreview.com/news/who-gave-china-veto-power-over-american-scientists-joining-covid-origin-investigation>

<https://www.sundayguardianlive.com/news/corona-leaked-likely-wuhan-institute-virology-experts>

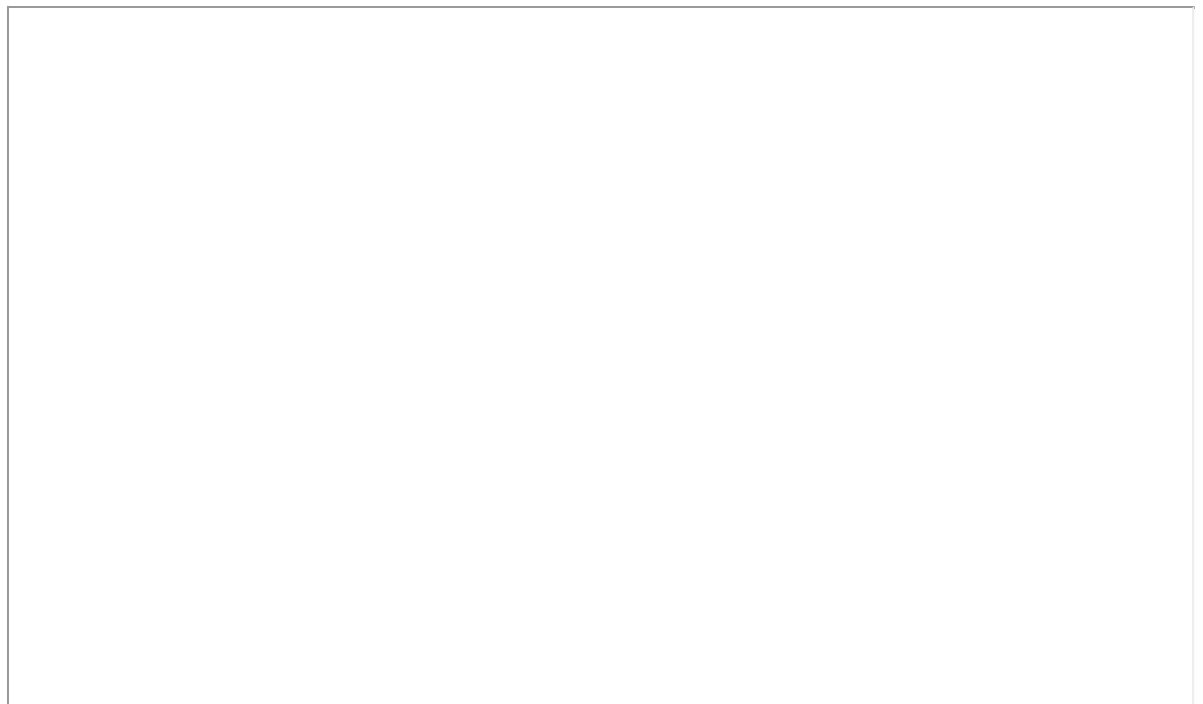
<https://www.documentcloud.org/documents/6884792-MACE-E-PAI-COVID-19-ANALYSIS-Redacted.htm>

<https://thebulletin.org/2020/06/did-the-sars-cov-2-virus-arise-from-a-bat-coronavirus-research-program-in-a-chinese-laboratory-very-possibly>

<https://www.gmwatch.org/en/news/archive/2020-articles/19392-expert-attacks-ecohealth-alliance-s-involvement-in-really-risky-bat-coronavirus-research-in-wuhan-labs?>

<https://nypost.com/2021/05/09/theory-that-covid-escaped-from-a-lab-may-not-be-far-fetched>

<https://nicholaswade.medium.com/origin-of-covid-following-the-clues-6f03564c038>





Shi's answers were coordinated with public information staffers at the Chinese Academy of Sciences, of which WIV is part, and it took her 2 months to prepare them. Evolutionary biologist Kristian Andersen of Scripps Research says he suspects Shi's answers were "carefully vetted" by the Chinese government. "But they're all logical, genuine, and stick to the science as one would have expected from a world-class scientist and one of the leading experts on coronaviruses," Andersen says. However, Richard Ebright, a molecular biologist at Rutgers University, New Brunswick, who from the early days of the pandemic has urged that an investigation look into the possibility that SARS-CoV-2 entered humans through a laboratory accident, was decidedly unimpressed. "Most of these answers are formulaic, almost robotic, reiterations of statements previously made by Chinese authorities and state media," Ebright says.

<https://www.sciencemag.org/news/2020/07/trump-owes-us-apology-chinese-scientist-center-covid-19-origin-theories-speaks-out>

THE INCUBATION PERIOD CONTROVERSY

Daszak's Zoonotic chirade was over after "an allied power" determined several lab technicians or scientists became contaminated with an enhanced SARS virus and brought it into Wuhan during its incubation period. (1.) Incubation time for COVID-19 between 2 and 10 days has been recorded by the W.H.O. The W.H.O. stated on February 10, 2020, at its press conference, that a very long duration of incubation can represent double exposure, 24 days was a specified point to be regarded in the sense of the study's key results. (2.) The Chinese National Health Commission initially expected a 10 to 14 days incubation period. (3.) The Centers for Disease Control and Prevention (CDC) from United States of America assumes the incubation period of 2 to 14 days for COVID-19. (4.) Doctors and health-care practitioners, of leading Chinese group DXY.cn predicts an incubation period of "3 to 7 days, and up to 14 days." (5.) In a report released on February 9, 2020, the incubation time was observed as long as 24 days (range from 0-24 days; average of 3 days) (6.) In a JAMA report released on February 21, 2020, a 19-day incubation period in infected patient has been identified, Hubei Province registered another case with an incubation time of 27 days, on February 22, 2020. An analysis sponsored by the Holland Ministry of Health and released by Eurosurveillance examined data for 88 identified travelers to and from Wuhan, which were identified as COVID-19 infected patients between January 20 and 28, 2020. It was calculated that the mean incubation period was 6.4 days. The incubation duration varied from 2.1 to 11.1 days. The 11.1-day maximum limit may be known as conservative. The incubation time greatly differs between the patients, according to a Chinese article reported by *New England Journal of Medicine* on January 30, 2020.

ECO-HEALTH ALLIANCE HEADQUARTERS



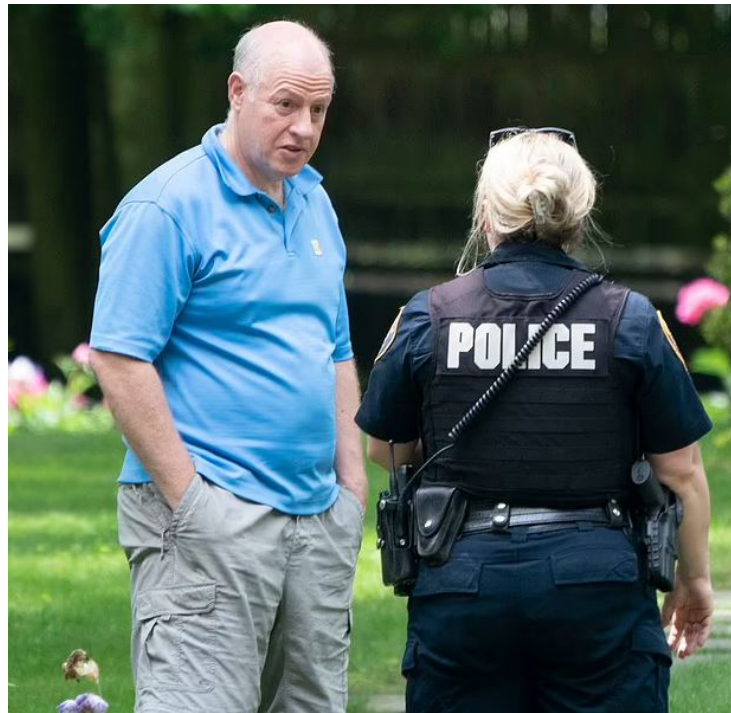


520 Eighth Avenue, Ste. 1200, New York, NY 10018 212.380.4460
WILL <https://www.youtube.com/watch?v=dfR-3vnuTlo&t=144s>

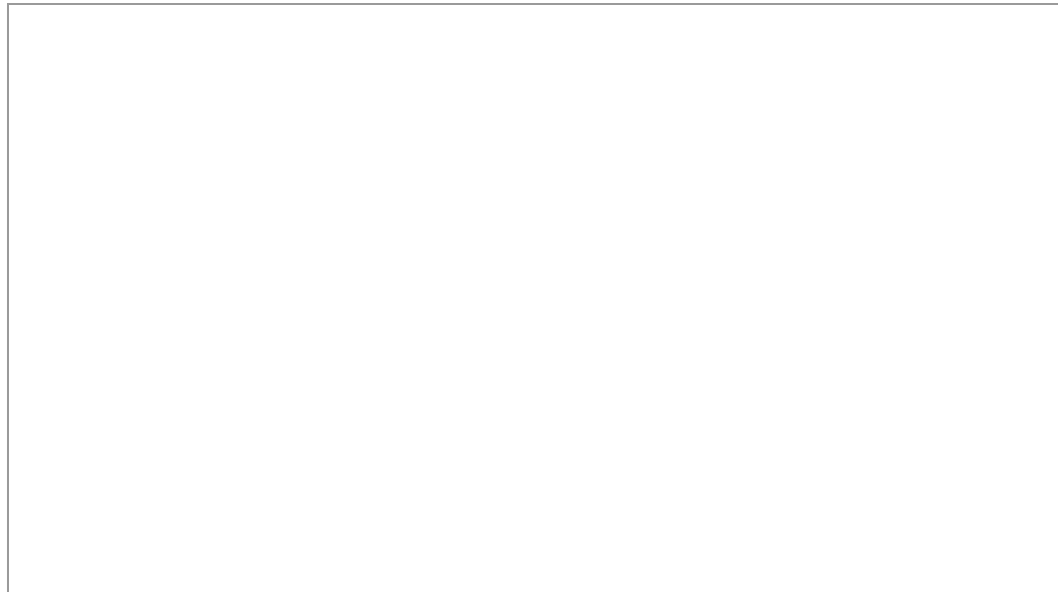
FIRST DEMONSTRATION AGAINST ECO HEALTH



DASZAK GREW RICH FROM HIS SCAM THAT NEVER PRODUCED A VACCINE



DASZAK EMAILS



Dear Randy:

As a member of the EcoHealth Alliance Board of Trustees, I would like to thank you and your wonderful colleagues for the generous vocal support and for the funding you are making possible for Peter and his research team. The entire board and the Alliance team are truly grateful for the extraordinary boost in morale you and your colleagues have provided. Peter and his team are doing critically important work on COVID-19 and its origin. In genuine gratitude, Rita.

Dear Ralph, Linda, Jim, Rita, Linfa and Hume, I've been following the events around the novel coronavirus emergence in China very closely and have been dismayed by the recent spreading of rumors, misinformation and conspiracy theories on its origins. These are now specifically targeting scientists with whom we've collaborated for many years, and who have been working heroically to fight this outbreak and share data with unprecedented speed, openness and transparency. These conspiracy theories threaten to undermine the very global collaborations that we need to deal with a disease that has already spread across continents. We have drafted a simple statement of solidarity and support for scientists, public health and medical professionals of China, and would like to invite you to join us as the first signatories. If you agree, we will send this letter to a group of around half-a-dozen other leaders in the field and then disseminate this widely with a sign-up webpage for others to show their support by signing up to its language. I will then personally present this at my plenary during the ICID 2020 conference in Malaysia in two weeks, with the goal of also getting widespread attention in SE Asia to our support for the work that our colleagues in China are undertaking. I sincerely hope you can join us. Please review the letter, and let me know if you are willing to join Billy Karesh and myself as co-signatories. Also, please confirm your title and affiliation that will be shown in the letter. We plan to make circulate this widely to coincide with a letter from the Presidents of the US National Academies of Science, Engineering, and Medicine, which will likely be released tomorrow or Friday. Thank you for your consideration and support of the scientific and public health community around the world! Cheers, Peter Daszak President EcoHealth Alliance 460 West 34th Street – 17th Floor New York, NY 10001 Tel. +1 212-380-4474 Website: www.ecohealthalliance.com.
NUMEROUS PAGES DELETED AFTER THIS.

From: Tara Hoda

Sent: Thursday, January 24, 2019 1:57 PM

To: rcolwell@umiacs.umd.edu; Victoria Lord

Cc: Anthony Ramos; Peter Daszak

Subject: Carnegie Corporation Contacts

Dear Dr. Colwell: It was so wonderful meeting you at the board meeting last week. As mentioned, we will be submitting a Letter of Inquiry to the **Carnegie Corporation under their International Peace and Security** portfolio. Our proposed project focuses on promoting a multi-sectoral approach and building capacity and partnerships for pandemic outbreaks and international health security processes in Western Asia. Our LOI is attached to this e-mail. You had mentioned you may have connections with the following people who are members of Carnegie Corporation's Board of Directors:

- 1) Jared Cohon
- 2) John DeGioia
- 3) Marcia McNutt
- 4) Judy Woodruff

For the Carnegie Corporation, it will greatly increase our chances of having our proposal considered if we have a point of contact. Would you be willing to put us in touch with one of the people above, or to directly send an e-mail letting them EcoHealth Alliance will be submitting an application? Any and all leads would be greatly

appreciated. Best, Tara

Tara Hoda Development Associate EcoHealth Alliance

I'm on a panel on biothreats...National Press Club, Washington, DC, Monday afternoon April 30...along with a roster of DoD, CIA, DHS, and other assorted luminaries. Anything I should say or comment on regarding EcoHealth, Peter?

CARNEGIE FOUNDATION CIA LITE: DCIA William J. Burns was president of the Carnegie Endowment for International Peace.

Mrs. Morris Hadley, another civic leader, whose husband was one-time head of the **Carnegie Foundation** and is now head of the CIA conduit Rubicon Foundation. Through his membership in the law firm of Milbank, Tweek, Hadley, and McCloy he has close association with John J. McCloy, once chairman of the board of Chase Manhattan Bank, former chairman of the Ford Foundation, past president of the World Bank, past U.S. High Commissioner to Germany and chairman of the board of the New York International House, a Rockefeller-backed institution dedicated to making the foreign student feel at home.

I think that many of EcoHealth Alliance's initiatives would dovetail well with Carnegie Corporation's International Peace and Security area of interest. EcoHealth Alliance's President, Dr. Peter Daszak, is the chair of the National Academies of Sciences' Forum on Microbial Threats, a member of the NRC Advisory Committee to the US Global Change Research Program, and has advised the Director for Medical Preparedness Policy on the White House National Security Staff on global health issues. He is also actively involved in the W.H.O. Expert group on Public Health Emergency Disease Prioritization.

Under the subject line, "No need for you to sign the "Statement" Ralph!!," he wrote to two scientists, including UNC's Dr. Ralph Baric, who had collaborated with Shi Zhengli on the gain-of-function study that created a coronavirus capable of infecting human cells: "you, me and him should not sign this statement, so it has some distance from us and therefore doesn't work in a counterproductive way." Daszak added, "We'll then put it out in a way that doesn't link it back to our collaboration so we maximize an independent voice."

ECO-HEALTH ALLIANCE FILED PURPOSES

Ecohealth Alliance integrates innovative science-based solutions and partnerships that increase capacity to achieve two interrelated goals: protecting global health by preventing the outbreak of emerging diseases and safeguarding ecosystems by promoting conservation. USAID PREDICT EMERGING PANDEMIC THREAT PROGRAM - assesses capacity and develops plans for the implementation of wildlife surveillance support. They develop models of disease risk and spread, implement a smart (strategic, measurable, adaptive, responsive, and targeted) wildlife surveillance strategy to identify and target high-risk wildlife in the region's most vulnerable to zoonotic disease emergence. Defense Threat Reduction Agency - Dept of Defense - serological bio surveillance for spillover of henipa viruses and filo viruses at agricultural and hunting human-animal interfaces in peninsular Malaysia. The objective is to enhance capacity within the Malaysia government to characterize the distribution of and detect spillover of novel and known henipa viruses and filo viruses, (both groups include high consequence zoonotic pathogens) in indigenous populations and farms in peninsular Malaysia. Current surveillance strategies for novel zoonotic viruses rely exclusively on molecular detection tools, but Nipah and Ebola viruses are present at low prevalence in bat species which makes infected individuals difficult to detect. By establishing a multiplexed serological assay developed to detect antibodies against any henipa and filo viruses, the government of Malaysia will more effectively be able to determine the distribution of these high-impact viruses in wildlife reservoirs and detect evidence of spillover in at-risk human or livestock populations. The most comprehensive investigation of the epidemiology and ecology of the RVF virus ever conducted. The project brings together a diverse group of experts from governmental, non-governmental, academic and private organizations, both domestic and international. the 2010-2011 outbreak of RVF in south Africa had a significant impact on the health of people, animals and the local economy. Thus, a better, more integrated understanding of the virus in the environment and in animal and human populations is critically needed to improve public awareness. a booklet explaining the risks of RVF and similar diseases was developed for distribution to study participants in the region. Rather than being a collection of independent science projects, this one health project integrates data collected from climate and weather, vegetation cycles, and mosquito studies to better predict outbreaks in South Africa. Evidence of RVF in animals and people is being collected to better understand exposure, with groups of people in occupations with high risk for rvf and flocks of sheep will be followed for approximately four years. the work is centered in the free state and northern cape provinces and includes the epicenter of previous RVF outbreaks within the 40,000km2 study region. Dr. Peter Daszak is President of EcoHealth Alliance, a US-based organization that conducts research and outreach programs on global health, conservation and international development. Dr. Daszak's research has been instrumental in identifying and predicting the impact of emerging diseases across the globe. His achievements include identifying the bat origin of SARS, identifying the underlying drivers of Nipah and Hendra virus emergence, producing the first ever global emerging disease hotspots map, developing a strategy to find out how many unknown viruses exist that could threaten to become pandemic, identifying the first case of a species extinction due to disease, and discovering the disease chytridiomycosis as the cause global amphibian declines.

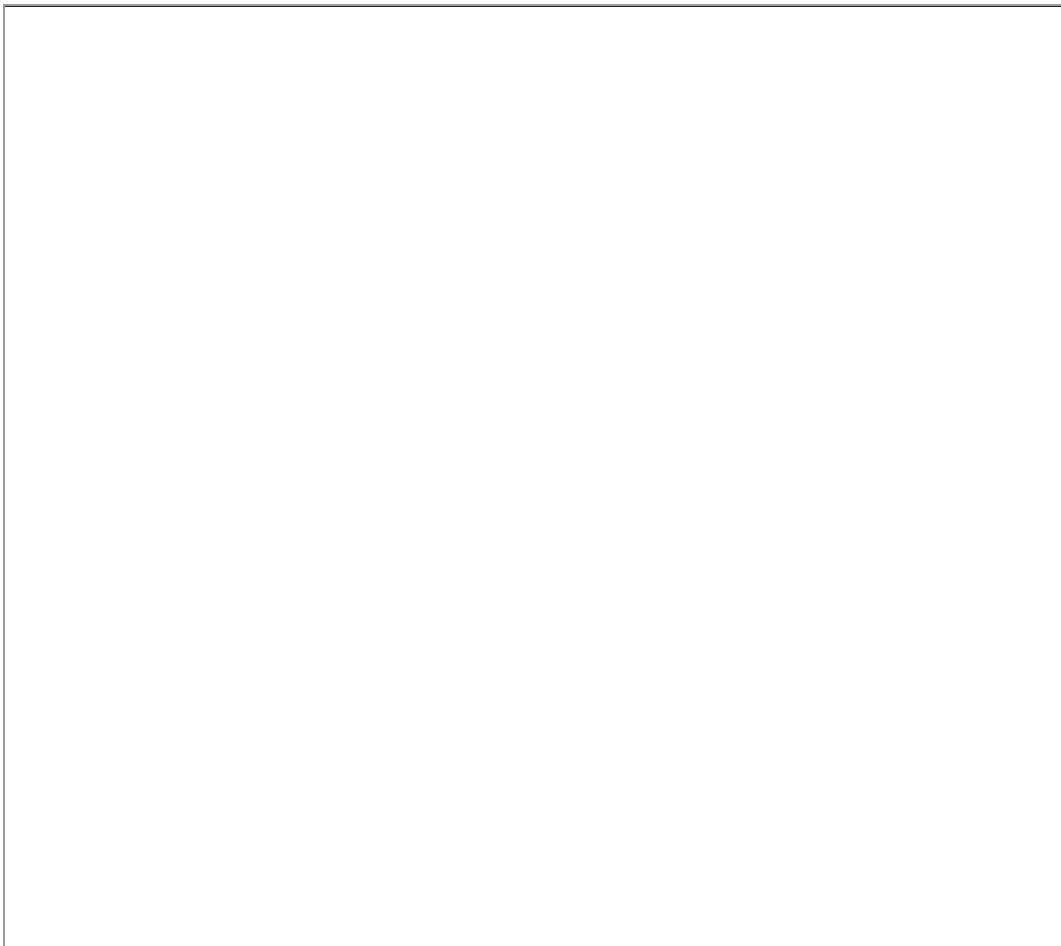
PREDICT is a consortium or partners working to enable global surveillance for pathogens that can spillover from animal hosts to people by building capacities to detect and discover viruses of pandemic potential. The project is part of USAID's Emerging Pandemic Threats program and is led by the UC Davis One Health Institute. The core partners are USAID, EcoHealth Alliance, Metabiota Inc., Wildlife Conservation Society, and Smithsonian Institution, along with a network of scientists and professionals in over 30 countries around the world. Contact us at predict@ucdavis.edu.

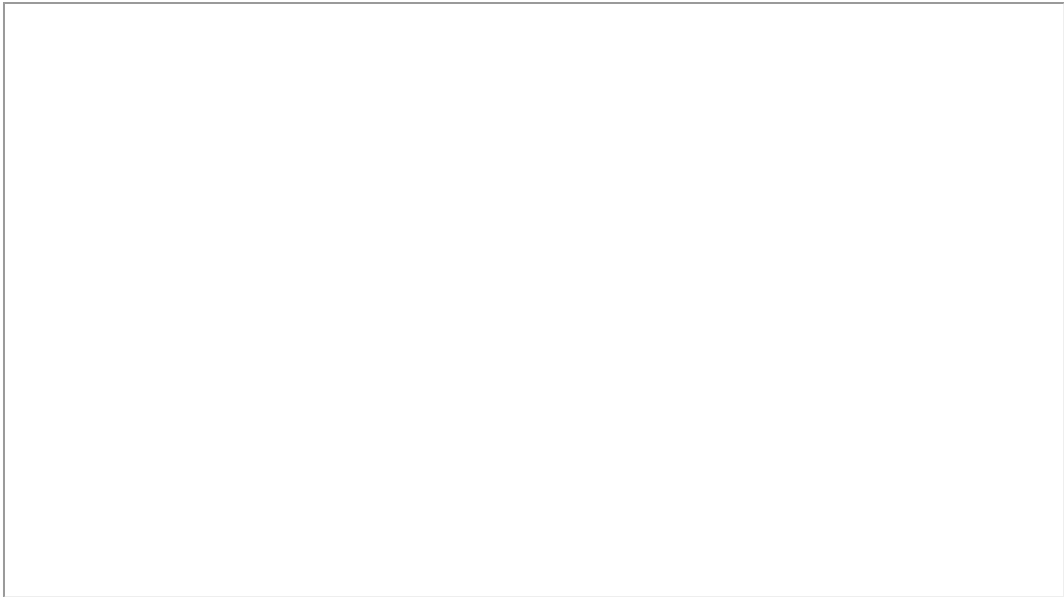
<https://www.linkedin.com/groups/13618543> The bubonic plague kept returning to Europe for centuries after it first emerged. But how that plague ended offers few relevant lessons for today's pandemic.



Researchers have been unable to find answers in animal studies of the bubonic plague. They have tried for decades to find general laws to predict how pandemics progress by infecting hundreds of thousands of mice with various viruses and bacteria, said Dr. George Davey Smith, professor of clinical epidemiology at the Bristol Medical School in England. The experiments went on year after year in England, Germany, the United States and Australia. All looked for ways to predict when and how an epidemic could end. [NYT](#) NYT's Carl Zimmer believes the plague didn't kill as many as it was first thought to have killed. The SARS outbreak of 2002 was caused by a bat coronavirus in China that infected some kind of wild mammal before infecting humans. Among the top suspects for that intermediate animal: the fluffy raccoon dog. "You could not get a better textbook example of disease emergence waiting to happen," Dr. Holmes, 57, said in an interview. Dr. Holmes has become one of the strongest proponents of an opposing theory: that the virus spilled over from a wild animal. With colleagues in the United States, he recently published tantalizing clues that raccoon dogs kept in the very iron cage he photographed in 2014 could have set off the pandemic. Dr. Holmes's Covid research has won him international acclaim, including Australia's top science prize. But it has also garnered claims that his research had been overseen by the Chinese military. His fellow researcher, Dr. Zhang paid a price for defying his country's information ban. The day after the genome sequence went live, his laboratory at the Shanghai Public Health Clinical Center was reportedly ordered to close for "rectification." Dr. Zhang later insisted to a reporter at Nature that the move was not a punishment, and that his lab later reopened. Dr. Holmes came under attack for his work with Chinese scientists. In May 2020, The Daily Telegraph, an Australian newspaper, linked him to the Chinese military with an article titled, "How the Red Army Oversaw Coronavirus Research." The newspaper based its claim on the fact that two scientists involved in the pangolin study had secondary affiliations with a Chinese military lab. Dr. Holmes, who said he never met the scientists, noted that they had helped with sequencing RNA from the pangolin tissue. [Daily Telegraph](#)

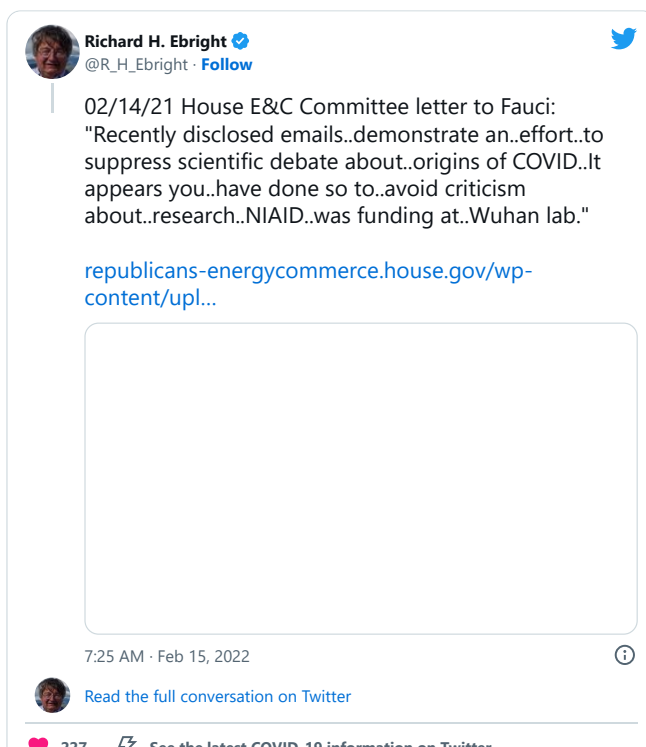
W.H.O.





[GUIDESTAR NON-PROFIT REPORT ON ECO-HEALTH ALLIANCE](#)

EBRIGHT TWEET





ANIMATION SHOWING HOW COVID PLUGS INTO ACE2 RECEPTORS








CHAPTER 41

PETER DASZAK'S TWEETS


**EcoHealth Alliance** 
@EcoHealthNYC · [Follow](#)



"Every single outbreak of a novel virus, somebody somewhere says, 'Well this has been manufactured in a lab.' ... We estimate there are 1.7 million unknown viruses in wildlife, so there's a lot of diversity out there and we need to be looking at that instead of pointing fingers."

 **Democracy Now!**  @democracynow


Despite all evidence pointing to the contrary, President Trump this week suggested the coronavirus originated in a Chinese lab. Zoologist and disease ecologist @PeterDaszak says that idea is "pure baloney," calling it a needless "politicization of the origins of a pandemic."





Hudson River Valley, NY

Dr. Peter Daszak | President of EcoHealth Alliance



10:47 PM · Apr 16, 2020




 87

 See the latest COVID-19 information on Twitter

[Read 6 replies](#)

**EcoHealth Alliance** 
@EcoHealthNYC · [Follow](#)



A recent Pew study found that one-in-three Americans believes a theory that the virus behind COVID-19 was lab released. There is no science to back this up.

vox.com

Why these scientists still doubt the coronavirus leaked from a Chinese lab
A Wuhan lab studied SARS-related viruses. But there's no evidence it discovered



Peter Daszak
@PeterDaszak · Follow



"Testing of samples from a Wuhan food market...failed to show links between animals being sold there & the pathogen. Gao Fu, director of China CDC said 'It now turns out that the market is one of the victims.'"

wsj.com

China Rules Out Animal Market and Lab as Coronavirus Origin
Chinese scientists in recent days said they had ruled out both a laboratory and an animal market in the city of Wuhan as possible origins of the coronavirus ...



Peter Daszak
@PeterDaszak · Follow



I'm glad the reporters at @nytimes recognized the incredibly fast work and open sharing of data from our colleagues at Wuhan Institute of Virology led by Zhengli Shi and Peng Zhou.

nytimes.com

As New Coronavirus Spread, China's Old Habits Delayed Fight (Publish...
At critical turning points, Chinese authorities put secrecy and order ahead of openly confronting the growing crisis and risking public alar...

2:21 AM · Feb 3, 2020 from New York, USA



[Read the full conversation on Twitter](#)

JOHN DASZAK'S TWEETS



John Daszak
@johndaszak · Follow



1) As many of you already know, my brother @PeterDaszak is one of the 15 "Experts" sent to China by the WHO to investigate the origin of SARS Cov2, the cause of the present pandemic and Covid-19 outbreak..



youtube.com

CNNi: WHO expert investigated Wuhan lab. CNN s...
A team of international experts from the World Health Organization are looking for the source of ...

2:27 AM · Feb 5, 2021



[Read the full conversation on Twitter](#)



55



[See the latest COVID-19 information on Twitter](#)

[Read 45 replies](#)



John Daszak
@johndaszak · [Follow](#)



What he says...



TIAN Wei @tianwei

🇨🇳 China state-affiliated media

"How outrageous is that?! They're fighting against the pandemic, yet others are accusing them of creating & spreading the virus?!" @PeterDaszak member of WHO-China team, fought back at unfounded accusations against his Chinese peers, while warning rumors might still linger. @WHO



7:35 PM · Feb 10, 2021



5



See the latest COVID-19 information on Twitter



From the Field to the Pharmacy: Fightin...



Watch later



Share

COVID-19 vaccine • Learn about vaccine progress from the WHO >



Dr. Peter Daszak
President, EcoHealth Alliance



Dr. Tillman Gerngross
Co-Founder and CEO,
Adagio Therapeutics

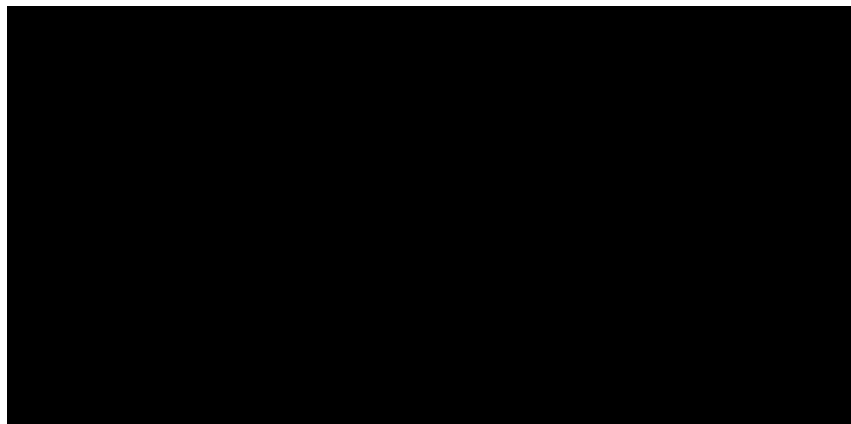


Clive Meanwell
CEO, Population Health Partners

Watch on YouTube



GERMAN VIDEO EXAMINES THE GoF / GoT Insanity





<https://www.ecohealthalliance.org/updates>

THE ORIGIN PAPER'S REFERENCE TO FURIN CANNOT BE FOUND

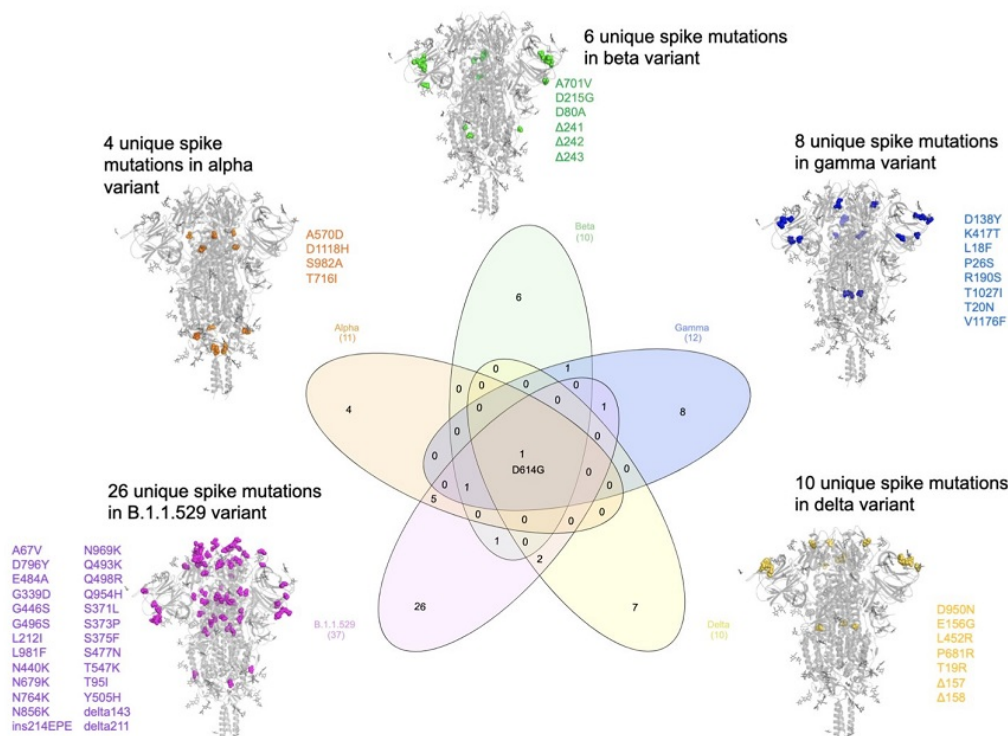
#SARS-CoV-2 also shows similarities to the four endemic human coronaviruses: HCoV-OC43, HCoV-HKU1, HCoV-229E, and HCoV-NL63. These viruses have zoonotic origins and the circumstances of their emergence are unclear. In direct parallel to SARS-CoV-2, HCoV-HKU1,

— A. J. Weberman (@AJWeberman) July 24, 2021

<https://academicinfluence.com/people/peter-daszak>

CHAPTER 42

OMICRON: HIT CONTROL+F AND SEARCH FOR "SPIKE" TO DISCOVER HOW DASZAK & DUPES MADE A CORONA VIRUS MORE PRONE TO MUTATION

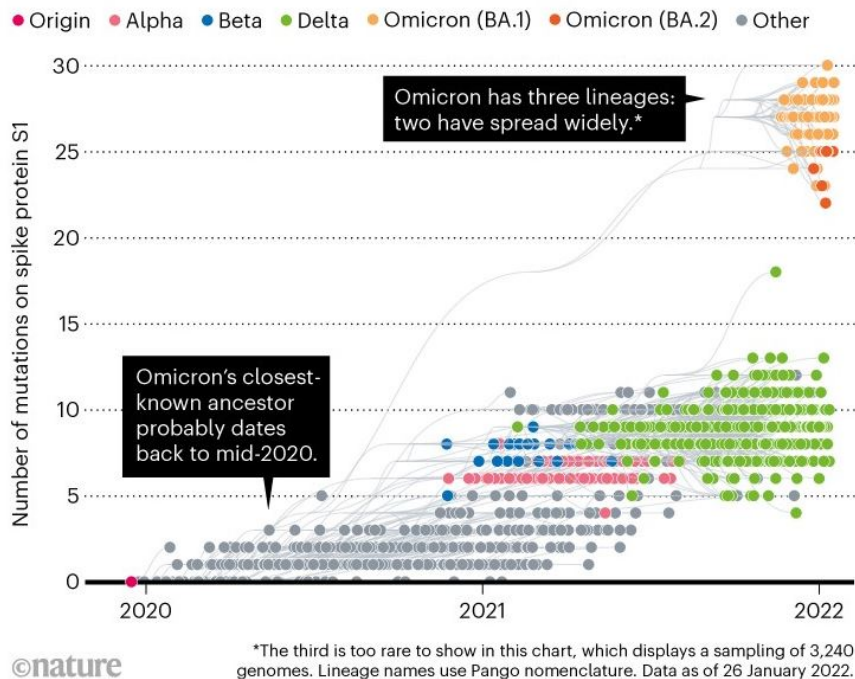


To date, under 2% of people living in Africa's low-income countries (LICs) have been fully vaccinated, and vaccination rates are still below 1% in many countries. For Africa's lower middle-income countries (LMICs), the figure is under 10%. Africa has produced AIDS, EBOLA and numerous other diseases. A continent of about 1.4 billion people has received just 404 million doses of vaccine, and only 7.8 percent of the population is fully vaccinated. Disease has always been a major export. [NYT](#) In South Africa Vaccine acceptance declined amongst White adults from 56% to 52%, while it increased from 69% to 75% for Black African adults. However, White adults were more likely than Black Africans to have been vaccinated (16% compared to 10%). [Human Sciences Research Council Johannesburg](#) Omicron has numerous mutations with potential to increase transmissibility, confer resistance to therapeutics, or partially escape infection- or vaccine-induced immunity. On November 26, 2021 WHO designated B.1.1.529 as a variant of concern, as did the U.S. SARS-CoV-2 Interagency Group (SIG) on November 30, 2021. On December 1, 2021, the first case of COVID-19 attributed to the Omicron variant was reported in the United States. As of December 4, 2021, however, the SARS-CoV-2 B.1.617.2 (Delta) variant was estimated to account for 99.9% of SARS-CoV-2 circulating in the United States. [CDC](#) Omicron is between two and four times more contagious than Delta, according to a Danish study that has not yet been peer reviewed. It's also better at evading the antibodies triggered by vaccines, which is why it's causing more breakthrough infections...Global tally of new Omicron coronavirus cases has for the first time passed one million per day on average. [NYT](#) No previous variant has spread nearly as fast as Omicron, with reported coronavirus cases rocketing from about 600,000 a day worldwide in early December to more than three million a day now. Madrid is pushing for Omicron to be treated more like the flu despite the virus still behaving as a pandemic. Jan. 11, 2022 LONDON — More than half of people in Europe could be infected with the Omicron variant of the coronavirus in the next six to eight weeks, the World Health Organization warned, amid

"a new west-to-east tidal wave sweeping across the region." "The region saw over seven million cases of Covid-19 in the first week of 2022, more than doubling over a two-week period," Dr. Hans Kluge, the agency's regional director for Europe, said at a news conference. The low rate of coronavirus infections, hospitalizations and deaths in West and Central Africa is the focus of a debate that has divided scientists on the continent and beyond. As of 9 February 2022, 11.1 million COVID-19 cases and 238,845 deaths were confirmed on the African Continent. To date, the pandemic has progressed in four main waves, with the most recent wave largely due to the Omicron variant circulating in a number of countries. However, reported data indicates a less severe disease profile in Africa compared to other regions globally: fewer cases, proportionally fewer patients with severe outcomes and death, and proportionally more asymptomatic cases. Some say it is because the population is younger due to a high death rate and other factors. [medRxiv and bioRxiv](#)

MOST MUTATED

The Omicron variant of the SARS-CoV-2 coronavirus has more mutations than any known predecessor. This chart shows mutations in the S1 subunit of the spike protein, which attaches to host cells.



Given the evident epidemic growth advantages of Omicron over all previously known SARS-CoV-2 lineages, it is crucial to determine both how such complex and highly adaptive mutation constellations were assembled within the Omicron S-gene, and why, despite unprecedented global genomic surveillance efforts, the early stages of this assembly process went completely undetected. [biorxiv.org](#) Does Omicron spread faster than earlier variants? Yes, in all likelihood. "The data out of South Africa suggest that the Omicron variant is spreading more quickly than Delta," Janet Baseman, an epidemiologist at the University of Washington, stated. The number of Covid cases is soaring in South Africa.

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INFORMATION FOUND AT COVID-19 RESEARCH INSTITUTE

THE FRENCH HELP WIV BUILD THE LEVEL 4 BIOCONTAINMENT LAB DESPITE DUAL USE CONCERNS

THE PROXIMITY FACTOR

PATIENT ZERO

TEXAS COLLEGES AND UNIVERSITIES IN BED WITH WIV THANKS TO FAUCI GRANT

IT'S NOT OVER UNTIL THE BAT LADY SINGS

SHI ZHENG LI CREATED THE COVID-19 VIRUS AT THE WUHAN INSTITUTE OF VIROLOGY

BATLADY MAKE BIG MISTAKE: SHE DID IT IN A LEVEL 2 BIOCONTAINMENT LAB, AND IT LEAKED OR SOMEONE GOT INFECTED IN THE LAB AND BROUGHT THE VIRUS BACK HOME.

SHI ZHENG LI WORK AT THE TIME OF OUTBREAK INVOLVED STUDYING CORONA VIRUSES ALMOST IDENTICAL TO SARS Co-V-2

SHI ZHENG LI CHRONOLOGY SHOWS SHE HAS A FINGER IN EVERY CORONA VIRUS EXPERIMENT

SHI ZHENG LI POST SARS-CoV-2 IN SCIENCE MAGAZINE

DESTRUCTION OF SARS-COV-2 SAMPLES

THE INTERVIEW WITH THE BAT LADY "COVID IS PUNISHMENT FOR AN UNSANITARY LIFESTYLE"

2018 SHI ZHENG LI WAS CREATING SYNTHETIC VIRUSES

SHI ZHENG LI 2015 EXPERIMENTS IN UNIVERSITY NORTH CAROLINA, CHAPEL HILL LAB PRODUCED NOVEL VIRUS MORE DEADLY TO OLDER PEOPLE JUST LIKE SARS-CoV-2 AND STIR DEBATE ABOUT GoF RESEARCH CAUSING A PANDEMIC 2020: NATIONAL INSTITUTE OF HEALTH SL-SHC014-MA15: MAN MADE VIRUS WHICH USES ACE2 RECEPTOR

THE ACE2 AFFINITY INDICATED A DESIGNER VIRUS

THE AUSTRALIAN STUDY: SPIKE PROTEIN OPTIMIZED TO BIND TO HUMAN ACE2

SHI ZHENG LI 2015 EXPERIMENTS SYNTHESIZING VIRUSES THAT ATTACK ACE2 RECEPTORS IN HUMANS WERE PRECURSORS TO CREATION OF SARS-CoV-2

2015: ISOLATION AND CHARACTERIZATION OF A NOVEL BAT CORONA VIRUS CLOSELY RELATED TO THE DIRECT PROGENITOR OF SARS: CREATION OF A VIRUS THAT CAN USE ACE2 AS RECEPTOR

COVID-19 STILL NOT FOUND IN NATURE

NEW YORK TIMES 9/20/2020 CHINA VIRUS STILL NOT FOUND IN NATURE

THE AUSTRIAN STUDY: IS CONSIDERING A GENETIC-MANIPULATION ORIGIN FOR SARS-COV-2 A CONSPIRACY THEORY THAT MUST BE CENSORED? ROSSANA SEGRETO UNIVERSITY OF INNSBRUCK INSTITUTE OF MICROBIOLOGY

PASSAGING

THE NORWEGIAN STUDY

SIR RICHARD DEARLOVE FORMER MI-5 DIRECTOR SUPPORTS NORWEGIAN STUDY

UNIQUE NEW FEATURE OF SARS-CoV-2 CALLED "UNEXPECTED INSERTION"

SHING HEI ZHAN, BENJAMIN E. DEVERMAN AND YUJIA ALINA CHAN, "SARS-COV-2 IS WELL ADAPTED FOR HUMANS

HUMAN ENGINEERING OF A POLYBASIC HA CLEAVAGE SITE MUTANT WAS EASILY ACCOMPLISHED

BTCOV/4991, RATG13, RMYN02 CLOSE BUT NOT INDENTICAL TO SARS-CoV-19

RICHARD EBRIGHT: THESE EXPERIMENTS HAS GOTS TO GO!

THE WET MARKET

VIRUS WAS NEVER FOUND IN ANIMALS AT THE WET MARKET OR ANYWHERE ELSE

CHICOM RE-ACTION DISINFORMATION CAMPAIGN

BOLTON AND TRUMP PAVE THE WAY FOR THE PANDEMIC

WORLD HEALTH ORGANIZATION

NEW WHO JUNKET

WHO DISPUTES THE FACT THE VIRUS LINGERS IN THE AIR INDOORS, INFECTING THOSE NEARBY.

CCP PROPAGANDA

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